

FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGA
 CCTGGTGCACCAACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCAGGCGCTCCCTGTGTGGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAACTGGCCAAGAAGCTCAAAGAGGCAGCATTGGAACCATCGATGGAATAATATTAAATTT
 GATCAGATGGGAAGATGGTTGTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCATTCCACCTATATGTAATTAGCAGGGAGTATTGGTTTAACAGCT
 TTGCTGCCATAGCAATCAGCAGAACGCCCTGTTCTCATGAACCTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTGTGGGAGGCCCTCCACTGTGGCCATGTGTGCCCCAGTGAAGAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCCCTGGGTCTCGTCTTTGTGCTCTATTGGGATCTATG
 TTTCTCCACCTACCACCGCTGGCTGGTGCCACTCTTACTCAGTGGCAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
 ACATTAATATATATTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACGAAAGAAAT**AG**
AAGTGACTCAGCTTCTGGCTTCTCTGTACATCAAATATCTTGTTTAAATGGGGCAGATATGC
 ATTAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGTGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCATGTTTGAGTGAATTTTAAATGTT
 TTGGTGAATGTGAAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAATTTAGCAAACCTGTGTTTGCATATTTTTTGGAGT
 GCAGAATATTGTAATTAATGTCATAAGTGATTGTGGAGCTTTGGTAAAGGGACAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGAAACAAAGTGGTCATTGTTACATTCATT
 GCTGAACCTTAACAAAACGTGTTTCATCCTGAAACAGGCACAGTGATGCATTCCTCTGCTGTTG
 CTTCTCAGTGCTCTCTTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTACTTTTGAATGTTTCAAAAGGAA
 ATAACTTTAAACTATTCTCAAGAGAAAATATTCAAAGCATGAATATGTTGCTTTTTTCCAG
 AATACAACAGTATACTCATG

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSPMEKIPKIDQMGRWFVAGGAAVGLGALCYGGLGSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLNMFMRGWSVTIGVTFAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLITLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
VGLGLFVSVLSLGMFLPTTVAGATLYSIAWYGGVLVFSMFLLYDTQKVIKRAEVSPLYGV
QKYDPIINSLMYSYMDTLNI FMRVATMLATGNNRKK

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCGGTGGCGCCACGTCGCCCGCTCTCCGCCCTTCTGCAT
CGCGGCTTCGGCGGGCTTCCACCTAGACACCTAACAGTCGCGGAGCGCGCGCGCTCGTGAGGG
GGTCGGCAGCGGGATCGGGCGGTCTTGTGCATCTTGGCTACCTGTGGGTGCGAAGATGTCGG
ACATCGGAGACTGGTTTCTAGGAGCATCCCGGCGATCAGCGCTATTGGTTTCCGCCGCCACCGTC
CGCGTCCCTTGGTCGGCAACTCGGCTCATCAGCCGCGCTACCTCTTCCCTCTGGCCGGA
AGCCTTCCCTTTATCGCTTTTACAGTTTGGAGGCCAATCAGTCGCCACCTTTTATTTCCCTGTGG
GTCCAGGAACCTGGATTCTTTTATTGGTCAATTTATATTTCTTATCAGTATCTTACGGA
CTTGAACAGGAGCTTTTGTATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTCCTCTGATCA
TGTCAGTACTTTATGTCTGGGCCAGCTGAACAGAGACATGATTGTATCATTGTGGTTTGGGA
ACACGATTTAAGGCTGCTATTTTACCTGGGTTATCCTTGGATTCAACTATATCATCTGGAGG
CTCGGTAATCAATGAGCTTATTTGAAATCTGGTTGGACATCTTTATTTTTTCCATATGTTCA
GATACCCAAATGGACTTTGGGAGGAAGAAATTTCTATCCACACCTCAGTTTTTGTACCCGCTGG
CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCGCTGCTAGCATGAGGCGGAG
TGCTGATCAGAATGGCGGAGGCGGAGACACAACCTGGGGCCAGGCTTTCGACTTGGAGACC
AGTGAAGGGGCGGCCCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
CACTTAACAACTGCGTCTTGGCTAACACTGTTGGACTGACCCACACTGAATGTAGTCTTTT
AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAATATAAGTGTTCACAAAGTTTCCAGAT
TCTCATCTCAAGTCTTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAACTGAC
TACATTTTTTGGTGTCTTCTCTTCTCCCTTTCCGTCTGAATAATGGGTTTATAGCGGGTCTT
AATCTGCTGGCATTTAGCTGGGCTGGGTCAACAAACCTTCCCAAAGGACCTTATCTCTT
TCTTGACACATGCTCTCTCCACTTTTCCCAACCCCACTTTGCAACTGAGAAAGGTTG
CCCATAAAATGCTCTGCCCTTGACAGGTTCTGTTATTTATTTAGCTTTTGCAAGGCTGGTC
ACAACAATCATATTACGCTTATTTTCCCTTTTGGTGGCAGAACTGTACCAATGAGGGGAG
AAGACAGCCACGGATGAAGCGTTTCTCAGCTTTTGGAAATGCTGCTGACATCCGTTGT
AACCCTTTGCCACTCTTCAGATATTTTTTATAAAAAAAGTACCACTGAGTCTAGGAGGCCA
CAGATTTGGTTATTAATGAGATACGAGGTTGGTGCTGGGTGTTTGTTCCTGAGTGAAGTGA
TCAAGACTGTAGTGGAGTTGCAGCTAACATGGGTTAGGTTTAAACCATGGGGGATGCACCCC
TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
TAGGAGGATCCAGATCAAGTTGGCTACAGGAGATGCTCTCTTTGAGAGGTCCTGGGCAATTG
ATTCCCATTTCAATCTCATTCTGGATATGTGTTCATTGAGTAAAGGAGGAGACCCCTATA
CGCTATTTAAATGTCACCTTTTTTGCCTATCCCCCGTTTTTGGTCAATTTCAATTAATGT
GAGGAAGGCGCAGCTCCTCTCTGCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGGGGTGTGTTA
TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCACTTAAATACCCACAGCTTTTTT
TCGTAGGTGGGCTTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAGTTTTTGAAGGCCA
TGCTTTTTTACACAGTTATTTTTATTTATGACGTTATCTGAAAGCAGCTGTTAGGAGCAGT
ATTGAGTGCTGTGCACCTTTGAGGCAACTAAAAAGGCTTCAACAGCTTTTGTATCAGTTTCTT
TTCAGGAACATTTGTGCTTAAACAGTATGACTATCTCTTCCCCCACTTTAAACAGTGTGAT
GTGTGTTATCTTAGGAAATGAGAGTTGGCAACAACCTCTCATTTTGAATAGAGTTTGTGTG
TACTCTCCATATTTAATTTATATGATAAAATAGGTGGGGAGAGTCTGAACCTTAACTGTCA
TGTTTTGTGTGTCATCTGTGGCCACAATAAAGTTTACTTGTAAAAATTTAGAGGCCATTACT
CCAAATATGTGTGACGTACACTCACTTGTACGGCGTGGAGACTCATTTGTATGTATAAGAATA
TTTTCTGACAGTGAGTGAACCGGAGTCTCTGGTGTACCCCTCTTACCACTGAGCTGCCTGCGAG
CAGTCATTTTTTCTTAAAGGTTTACAAGTATTTAGAATTTTTCAGTTTCAGGCGCAAAATGTTT
ATGAAGTTATTTCTCTTAAACATGGTTAGGAAGCTGTAGACGTTATTTGATTTTGTCTGGATT
ATGTTCTGGAATAATTTTTTACCAAAACAGCTATTTGAGTTTTGACTTGAACAGGCAAAACA
TGACAGTGGATTCTCTTTACAAATGGAAAAAAAATCCCTATTTTGTATTAAGGACTTCCC
TTTTTGTAAACTAATCTTTTTTATGGTAAAAATGTAAATTAATATGCAACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLGSLSPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWQGQFRL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTGCCATAGCGACCATTTCGCATTAACTGGTTG
 GTAGCTTCTATCTCGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCCTAACCGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCTGTGCC
 CCTTTGGGCGGG**CATG**GCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGAGAGCATCG
 CGGGTTCCTGCGAGGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTCCCTTGTTTTGTATGATGAAGAAGAAAGCAAATGACCTATACAGAGATTCT
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCACTGACCTTGAAACAGAGAGATGAAAATCCT
 GAGGGAAGTCTCTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAGGAAAA
 AACAGTTATCAGAGGCTAAAAAGAGGCCACAGTGCATTCCAGTGAAGTGCATAATG
 AATAATTCCCAAGGGATGGTGAACATTTGCACACCCACCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGAAGGTCTGAACTTCCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCTGGCTTAGAGCATGCGAGCATGAAGGACCAATAGCAAAC
 TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAACTCAAAGAAGAAGTTATTAATAAG**TA**
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEDEVEWVESIAGFLRGPDWSIPILDFVEQKCEVNCCKGGHVITPGSPPEPVILVACVP
LVFDDEESKLTYTEIHQEYKELVEKLLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAADFTIFKAMMVQKNIEMLQAIIRIIQERNGVLPDCLTDGSDVVSVDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

GGGCACAGCACATGTCAAAGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGGAATACAAAGAACCTAGTTGAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAGAAGCATGCACCTCTCCCTTGCAAAGACCCATACATCACAG
GCCATTTTGCACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTTAACCGTAGGCTGCTGATGTGGTCACTGACCTTGAACCGAAGAGATGAAAT
CCTGAGGGAAGTCTCTAGAAATCAAAGAGGAATATGACCGAGAA

[illegible]

CGCTGGTTTTTGTCTTCGCAATAGGCGGCTTAAGGGAGGGGCTTTTTGCCTATACCTACTG
TAGCTCTCCACAGTATGGACCCATAAGGCTACTGCTGTCTACCTAGGGGCTAGACAGTTACTG
TCTCAGCTTCAGATGTGCGTCTCTTCCATAGAAGCTCTTCTGAGGAGGTAATTAAAAAAC
AGTGGAAATGGAAGAAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTTGCAACAATGTATAC
ATTCCTGCTGATGGTCCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
TCGCCAATTGAAGAAACAAAGTATGATTATCTTCCAACACTACTGTGAATGTGTCTCAGAACTG
GTGAAGCTAGTTTTCTGTGTGCTGTGTATCTGTGTTATAAAGAAAGATCATCAAAGTAG
AAATTTGAAATATGCTCTCTCGGAAGGAATCTCTGTGATTTTCATGAAGTGGTCCATCTCTGCC
TTCTTTATTTCTCGTGAATTCGTTGTCTCTATGCTCTGCTATCTTCAACAGCACT
GCTGTATCTCTTCAAAATTTTTAGCATATTAACAACAGCTCTTCTATCAGATAGTGTCTGAA
AGGCGCTCTAACTGGATCCAGTGGCTTCCCTCTGACTTTATTTTGTCTATTGTGGCT
TGACTGCCGGGACTAAACTTTACAGCACAACCTTGGCAGGACGTGGATTTTCATCAGATGCC
TTTTTCAGCCCTTCCAATTTCTGCTCTTTTCAAGAAGTGTGTCGCCAGAAAGACAATTTG
TAGACAAAGGAATGGACTTTTTCTTGAAGCTAAATGGAACACCAAGCCAGCGATTTTCAGTC
ACATCCGCTCTGGCATGGCCATGTTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
AATATCTATAATGAAAGAGTCTAGGAAGGGGGAACAGCTCACTGAAGACATCTTCATACA
GAACAGCAAACTCATATTTCTTGGCATCTGTTTTAATGGGCTGACTCTGGCCCTCAGAGA
GTAACCGTGATCAGATTAAGAAGTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
CTTATTTTTGTAAGTCATTCAGGGCCCTTTAGTGGCTTTTCATCTGAAGTTCTCTGGATA
CATGTTCCATGCTTGTATGGCCAGGTACCACGTGCTATATCACAAAGTGTCTGTCTCGT
TCTTTGACTCTCAGGCCCTCCTCGGAATTTTTCTTGAAGCCCATCAGTCTCTCTCTATA
TTTTATTATAATGCGCAGCAAGCTCAAGTTCTCGGAATACGCACCTAGGCAAGAAAGGATCCG
AGATCTAAGTGGCAATCTTTGGGAGCGTTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
CAAAACCCAAAGATGTAGTGAGTCAGATGAAGATCTTTTAACTCTGGTACCCACATAGTTTGA
GCTCTCTTGAACCTTAATTTTTACATTTACAGTTTGAATTTTATCTTTTTCTACTTGATA
AACCAGAAATGTTTCTAAATCCTAATATTTCTTGCATATATCTAGCTACTCCCTAAATGGTT
CCATCGCAAGGCTTAGAGTACCCAAAGGCTAAGAANAATCTAAAGAACATGATACAGGAGTAACA
ATATTGAAGAATTCATTAATATCTCAGTACTTGATAAATCGAAAGTATTATGTGCGAGATTAT
TTTTCTTGGCCTTCAAGCTTCCAAAAAATCTGTAATAATCATGTTAGCTATAGCTTGTATAT
ACACATAGAGATCAATTTGCCAAATATCACAATCATGTAGTCTAGTTTACATGCCAAAGT
CTCTCTTTTTACATATATAAAGCTAGGTTGTCTTGAATTTTAGGCCCTAGAGATAGT
CATTTTGAAGATTAAGAGCAACGGGACCTTTCTAAGAACTGTGGTTGAAGGCACTAAATAC
CTGGCCATACCATATGTTTTGGGATGATGTAGTCTGTGACATTAATTTTGTGCTGAAGAAGCAGT
TTCTCAGACACAACATCTCAGAATTTTAAATTTTATAGAAATTCATGGGAATTTGGATTTTGT
AATAATCTTTTGTATGTTTTAAACATTTGGTTGCTTCTAGTACCATAGTACCCTGTATTTTA
AGTCATTTAAACAAAGCCAGCTGGGGCTTTTTCTTCCAGTATTGAGGAGAAAATCTTGAT
GTCATTACTCCTGAATTTATTAATTTTGGAGAATAAGAGGGCATTTTTATTTATAGTTACT
AATTCAGGCTGTGACTATTTGATATCTTTCCAAGGATGGAATCTGGCTTCAGAATCATAC
CAGATGTGTCAGTAGAGCTGATGCCTAGGAATTTTTAAGGGATCTTTCAAAGGATCACTT
AGCAAAACACATGTTGACTTTTAACATGATGATGAATATTAATCTCTAAAATAGAAAGACC
AGTAATATATAAGTCACTTTACAGTGCTACTTCACATCTAAAAGTGCATGGTATTTTTCAGT
GATTTTGCATGCAAGCAGTTAACTCTGTAAGTAGAGAAGTCAGGTGATAGATGATATTAA
AAATTAGCAAAACAAAGTGACTGTCTCAGGGTACAGCTGGGTGATGATGAAGAGTGGG
CTTTAAGCTGGCAGGCTGTATGTTTTACAGACTACCATCTGAATATGACCTTTATGTTGT
CATTCTCAGAACTTATACATTTCTGCTCTCCTTCTCCTAAGTTTCATGCAGATGAATATA
AGGTAATATATCATATATATAATCATTTGTGATATCCACAATAATATGACTGGCAAGAATTG
GTGGAATTTGTAATTAATAATTAATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKDKHQSRLKYASWKEFSDFMKWSIPAFLYFLDNLI VFYVLSYLQPAMAV
 IFSNFSIITALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGFHHDAFF
 SPSNSCLLFRSECPKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSAFSVALI
 FVTAFAQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFI
 YNASKPQVPEYAPRQERIRDLSGNLWERSSSGDGEELERLTKPKSDESDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGGCTTAGAGGGAGGGGCTTTTTCGCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATAAAAAACAGTGGGAATGGAA
AAACAGTGTCTAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATACATTCTGCTAGG
TGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACCTACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCTATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTC
TGGATAACTTGATTGCTTCTATGTCCTGTCTATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGTGTAAGAGGCGTCTAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGGCCGGCTTGGCTAGCGCGCGGCGGCC
 GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGCGAGGAGCAT
 CCCGCTTACCAGGTCCCAAGCGGCGTGGCCCCGGGGTCATGGCCAAAGGAGAAGGCGCGGAG
 AGCGGCTCCGCGCGGGGCTGCTACCCACAGCATCTCCAAAGCACTGAACGCCGGGCCA
 GGTGAAGAAAGAACCGAAAAAGAAGAAACAAGTTGTCTGTTTGCACAAAGCTTTGCTATG
 CACTTGGGGGAGCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCTTCAGATCTAC
 CTATTGCAAGTGGCTCAGGTGGGCCCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCGGAGC
 CTGGGATGCCATCACAGACCCCCCTGGTGGGCTCTGCATCAGCAAAATCCCCCTGGACCTGCC
 TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCCCTGGCGCTATTGCTACTTCTC
 ATCTGGTTCGTGCCGACTTCCACACGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
 CTTTGAAACAATGGTCAGTGTTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
 ACCGAGCAGACTGAGCGGGATTCTGCCACCGCTATCGGATGACTGTGGAAGTGCTGGGCAC
 AGTGCTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCTTGTTCACAG
 ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACATGGCACCACCTTCACAC
 AGGGAAACGCAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTG
 TGCTGTCTCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
 AGCCAATCGCCTACTTCCGGGGCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACTT
 ATTACTGGCTTCTCTTCACTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGT
 TTGCACCTACACCTTGGGCTTCCGAATGAATTCAGAATCTACTCCTGGCCATCATGCTCT
 CGGCCACTTTAAACCATTCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
 GTATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAA
 CCTCATCTATTACATATCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTAC
 TACCCTGGTCCATGCTGCCGTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
 GGAACCGAGCCCATCTTCTTCTCCTTCTATGCTTCTTCCACCAAGTTTGGCTCTGGAGTGTC
 ACTGGGCATTTTACCCCTCAGTCTGGACTTTGACGGGTACCAGACCCGTGGCTGCTCGCAGC
 CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCCTG
 CTGGGCCGTGCTCTTCAAATGTACCCCATGATGAGGAGAGGCGGGCGGCAGAAATAAGAA
 GGCCCTGCAGGCACGTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
 AGCTGGCTAGCATCCTCTAGGGCCCCGCCACGTTGCCCGAAGCCACCATGCAGAAGGCCACAG
 AAGGGATCAGGACCTGCTCTGCCGGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
 CTGAAGACTCAAGGAGGTGGCCAGGACACTTGTGTGCTCACTGTGGGCGGGCTGCTCTG
 TGGCCTCTCTGCTCCCCCTGCTGCTGCTGTGGGGCCAAGCCCTGGGGCTGCCACTGTGAATA
 TGCCAAGAGCTGATCGGGCTAGCCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
 TAATTAATAACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGTCTGTGAGCTA
 TTAATGTTATTAATTTTCATAAAAGCTGGAAGC

MWLRWALSIFPSSCLMAEFGMPSQTPWWASANPPGPAWVALCPGSSSPRPWPSLPTSSSG
SCPTSHRTARPIGTCFSIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYRMTVEVLGTVL
GTAIQGGIVGQADTPCFQDFNSSTVASQSANHTHGTTHSHRETQKAYLLAAGVIVCIYIICAV
ILILGVREQREPYEAQQSEPIAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVEGNFVLFT
YTLGRNEFQNLLLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLI
ITYAVAVAAGISVAAFFLPWSMFLPDVIDDFHLKQPHFHGTEPIFFSFYVFTKFKASGVSLG
ISTSLDFAGYQTRGCSQPRVKFTLNLMLVTMAPIVLILLGLLLFKMYPIDEERRRKNKKAL
QALRDEASSGCSSETDSTELASIL

FIGURE 13

GGGAAACGCAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TACTGGCTTCTCTTCACCTCCTTGGCTTTCATGCTGGTGGAGGGGAACCTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCTTCAGCCCTTGTAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGCTACTTGAATACTGAGTTGTTTAGG
 ACTTCTATTGTGGCAAACCTCCAGAAAAACAACCCTTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTTCAGACCATCCTTTCCTACCAAATG
 CAGCCCCAAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTTGCACAGTGGCAATTTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAAATGGTCTATGTCAATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCGTGA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTTACATGGATTAAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCCAGAGATATTTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGATTGGGAAAGGTTACAGAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCCTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAGAAGCCATTTGATAGATTATTTCTAAAGGATATCATCAAGAAGACTA
 TTAAAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAGACTATG

MWWFQQGLSFLPSALIWTSAAFIIFYITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
AAVLICIAITYVRKQVHALSPEENVIIKLNKAGLVGLTGLSCLGLSIVANFQKTTLFAAHVSG
AVLTFGMGSLYMFVQTILSYQMOPKIHGKQVFWIRLLLVICVGSALSMLTCSSVLHSGNFG
TDLEQKLHWNPEKDKGYVLHMITAAEWSMSFSFFGFFLTYYIRDFQKISLRVEANLHGLTLYD
TAPCPINNATERPRLSDI

FIGURE 16

CGGACGCTTGGGCNGCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCTTTCCACAAAAGCTAATTGAGTACACGTTCTGTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

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FIGURE 17

CCCACGCGTCCGCCCGCCGCTGCGTCCCGGAGTGCAAGTGAGCTTCTCGGCTGCCCGCGGG
 CCGGGGTGCGGAGCGAC**ATG**CGCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGCTGTCGACGCGACTGCCCGCGGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCCTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCTA
 CCTCTACAAACAGGGCTTTGCCATCCCGGCTCCAGCTTCCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTGGCAAACAGTTGGTGGTGTCTACTTTCTCTGATAAAGT
 GGCCCTGCTGCAGAGAAAGTGGAGGAGAACAGAAACAGCTTGTTTTTTTTCTTATTGTTTT
 TGAGACTTTTCCCATGACACCAAACCTGGTTCTTGAACCTCTCGGCCCAATTCGAACATT
 CCCATCGTGCACTTCTTCTCTCAGTTCTTATCGGTTTGATCCCATATAATTTTCTCTGTGT
 GCAGACAGGGTCCATCCTGTCAACCTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
 TCTTAAAGCTGTGGCCATTGCCATGGTGGCATTAACTCCTGGAACCTCATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACAGTAGAAAAGA
 CACAT**GA**TCTGGATTTTCTGTTTGGCACATCCCTGGACTCAGTTGCTTATTGTGTAATGGA
 TGTTGCTCCTCTAAAGCCCCTCATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGTATTACATCAGGT
 TTTCAAACAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAATGCTGTTGT
 GGCCGGGCGCGGTGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTC
 ACAAGGTCAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 AAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCACTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEEAGGRSLWFPSDLAELRESEVLREYR
 KEHQAYVFLFCGAYLYKQGFAIPGSSFLNVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPFDKVALLRKVEENRNSLFFFLLFLRLFPMTPNWFLNLSAPILNIPVQFF
 FSVLIGLIPYNFICVQTGSILSTLTSLDALFSWDTVFKLLAIAMVALIPGTLIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCGAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGGACACGTGGTTTCCGAAGTCCAGCTCAGAA
TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGATCTTGTCTGCCAACGAGATCAGCA
TTTATGACAACTTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
CCCCCGCAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
TGCTCACTGCCTACTTTGTGATTCAACCTTTTCAGCCCATTAGCACCTGAGCCAGTGTCTTCT
GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCTTGGCCATTGCCAA
GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCCCTTTC
CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
AACTGCACTGGCTGTGCCAGAAAACACCTGAAGGTGATGTCTCTGGAAGACGCCCCCAAGGAA
ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTTGGAGGAAGAGATTC
AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
TGGTGGCGCTGCTTTCTGAGCGGTGGTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
CAGATCACAAATGTTACGTGAGCTTTTCTGTTTTCTCACTCACCTGCCATTTCCAAAAGATG
CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
ATGCCTGACCTATTTATCATTTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
GTGCCGAAGACATTGTCACTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCTG
ACACCACCCACTGGAAGGTTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCTATCTGCGAT
GGAACCGCTTTCTCAGAAGTGTAGGAAATAGAACTGTGCACAGGAACAGCTTCCAGAGCCGA
AAACCAGGTTGAAAGGGGAAAAATAAAAACAAAACGATGAAACTGCAAAAA

MDLAANEISIIYDKLSETVDLVRQGTGHCQGMSEKATIEKFRQLLEKNEFQRPFPQYPLLIIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSLIHHTRLMSLPIAKKYMSENKGVP
HGGDEDRPFPDFDPWNTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIIQHFLCKQYPEATEGFVSEGGFAKWWRCFIPWFWFFFPYPPWRRLNRSQMLRELFPV
FTHLPFDKASDLNKCSEFLHPEFVGSGMKMHKMPDLFIISGEAMLQLIIPFQCRRHQCVSAMP
IEPDPGIVYDTHHWKVYIARGVQPLVLGDTAFSEL

CCACGGTGTCCGTTCTTCGCCCGGGCGGACAGTGTCCCGAGGCGGGAGGAGCCCGAGGGGCGC
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCAGTTCTCAGCCGTTCAAGTTGTGATC
AAGGGACACGTGGTTTCCGAAC TGCCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTATGACAAACTTTAGAGACTGTTG
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTGAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAACTGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTTGATAAGGTTTCGACACCTTGGGATTATCTGCTCACTGCTACTTTGTGATTCAAC
CTTTACGCCCTTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

CACGCGGTTCGCGCCCTCGGCTCCGGCTGAACACCTTCTTCTTTGGAGCTCAGCACTGATGAGG
 CAGGTCGCCCACTTTCAGCTGCAGCAAGCTGCGCAGCTGCAGAGCGTGCTCTTGCTGCTGTG
 CCACCTGTTGCGCACCTGTCGTACAGCTGCTATGACGCGCTGCGAGTCTGCACTGGGACACTGCC
 CTCTCTGCCACCCACCAATTCGCGAGCCCACTCTTTTGAAGACTTCAGGGTCTTTGTGGCCA
 CCGCCGAATGGCGGCCACTTTCATCGACAACACAGGTACAGCCAACTGATGCTCCAGGTTCGAAATG
 SACACGTAAGCTCTAAGAGCCACGACCTTATGTTCAGGTTTCTTGGAAATGCTGCTCTATGACATGCT
 TATGACATAGTGGCGAGCGGCGCAGTGGGAGCGCGCCAGAGATCGTGGGCGCTTCACGAGGCT
 TGGTGTCTGGAACCTCGCGCAGAGGCGGGCGCGCTGGAGGGGCTACGCTACACGCGAGTGTCTG
 AAGCAGCAGGCAACGCGACGACTCATGTGGCCTGCTGCACTGGGGGGCGCTGTGGCGCCAGCG
 CGCCAGCCCATGTGGGGCGCTGGGCGCTGAGGGAACACTCCCATCCCGCTGGAAATGTCCG
 GCGCGGACGACATATTCAGCATCGTCTGAAGCTGGTGGCCAAACCATCACTTCGACCTTCAC
 CTCGAAGCGAGCGCTCTCCGAGACAATCTGGGTGAGGTTCCCTCGACACCAGGAGGAGGCT
 CTCACTGCTCTTGGCAGTGAACAAAGAGGCCAAAGTAGCAACCCACCGAGTTGCTGCAAG
 AGGCACAGCTCGCGCAGGACGAGCTGGTGCATGCTGGAGACCCGATGGAGCGAGCAGACATG
 GATGAGCAGCTTGAGAAGCTGGTGCTCTCGGCCGAGTCGCACTGGTGCAGGTAGTGGCGCT
 GGTCCGAGGGCTGTGGAGGTTCACCAACGAAATGTATCTACTTACGATGGCAGCACTGAGC
 GGTCTGGAAGAGCGAGGAGGAGCTACGGCTATGATTTTCGGCGGCCACTGGCCGAGCTGCGTGTGG
 GTCCACTCTCGCGCGTTTCAACCTCGCGCTTCAGCACTTGAGCTCTTCTTTATCGATCAGGC
 CAACACTCTTCTCAACTTCATCATGAAGTGGGCGAGCCACCGCACTCATCTCTAGCCAGA
 CTCGAGACCCCGAGCTGGGCCCATCCCAACCCCATACCGAGTACGGAACACAGGTGTACTCG
 TGGCTCTCGCGCTACGGCGCCCCCTCTCAAGGTACTAAGACGCGCTCTCCCCCGAGGAGAT
 GCTCGGCTGCTCAGGCTTACCCGAGAAATGGGTACAGGCTGAGATATCTCAACTCTCGAGTACT
 TGATGCACTCAACACCTTACGGGGCGGCACTACAATGACTGTCTCAGATACCTGTGTCTT
 CCTGTGGTCTCGCAGGACTACTGTGTCCCAACCTCGGACCTGACCAACCCAGGCGTGTTCGG
 GGACCTGTCTAAGCCCATCGTGTGGTGAACCCCAAGATGCCAGCTCGTGAGGGAGAATG
 ATGAAGAGTTTGGAGGCCAGCAGGGACCATGCAAGTTTCACTATGGCACCCACTACTCC
 AATGCAGCAGGCTGTGATCACTACTCTCCGCGTGGAGCCCTCACTCTCCTGCAAGCTGCA
 GTTCGCAAGGTGGCGGCTTTGACTGTCTCGACCGGCACTTCACTGAGTGGCGGCGAGCTGG
 AGGCAAGCGCTGAGAGCCCTCGGATGTGAAGAGCTCATCCCGAATTTCTTACTTTCTGT
 GACTCTCTGGAGACACGAAAGCGTTTGTGACTGGGCTGTCTCCAGCTGACCACAGGAAGGT
 AGCTTGCTGGTGTGCTACCCCGTGGGCGAGCTCTCTGAGGACTTCATCAGCAGCAGCCGC
 AGGCTCTGGAATCGGAATATGTCTCTGCACACTACACAGCTGGATCGACCTACTTCTTGGC
 TACAAGCAGCGGGGGCGAGCCGCGAGGAGGCCCTCAATGTCTTATTACTGCACTTATGA
 GGGGGCTGTAGACCTGGACCATGTGACACATGAGCGGGAACGGAAGCTCTTGGAGGGCATTA
 TCAGCAACTTTGGGCGAGACTCCCTGTCACTGTGAAGGAGGCACATCAACTCGGCTCTCA
 CTTGAGGAGAACGAGCCCACTGCCCTTGACAGCGCTTGGAACCTAAGCTCACTAGACTCTTCAGCA
 CTTGGAGCAACTCAAGGCATTTCTTCAGAGAGTGAAGTGAAGTCCAGTGGGCTGTGGGCA
 CCCACAGCTGTTTGCCATCTGACCCGCAACATAAGCACTACTTTCAGCTTCAGCAAGACCCC
 ACCATGGGCAAGCCAAAGACGAGCACTGTGATGAGTGGCGCTGGGTGCCAGGAGTGTGTG
 GAGTGGCAAGCACTGGCACTGGCCCGGATGAAAGCTGTATTGACCGGTTGGCCACTGGG
 ATGGCAGCTCGGGGTGACTGCATACCCCGTGGAAAGCTGTTTGAAGCGCTCACTGCCAC
 TCTGTATGTAGTAACCTGCTTCTGCACTGGACACTCTTGGCATCTCACTCACTCAGGCTCCCG
 GGACACCAACGCTCATGTTGGTGTGGCGCTCTGCACTCAGGTTGTCTGTCACTAGGCTGGC
 CAACTCTGTGCAAGTCTGTGTATGGGATGGGCTCGAGTAGAGTGTGTGGCCATCAGCACT
 GAAGTGTGACATGGCTGTGTCTGATCTGAGGATGGAATGTGATATACACTGATTCAGCCG
 CGACAGTTTGTGTAGCGGCACTACGGCCTCTGGTGTGACACATTCCTTGGACCTATTTTGGACC
 TGGCATTTGGGTTCGGAAGGCGAGATGTGTGTACAGCACTCAGCGTGGGAAGCTCTTTGGGCG
 CAGGTCACTACTCTTCTGCACTGTATTGACCTCAATGGGAAGTGTGGGCTTCACTGCCCC
 GCGAGACAGCTACAGCCCTGACGGTGCAGAGGACTTTGTGTCTGGGCACCGCCAGT
 GCGCCCTTGCACTCTCCCAACTAACAACACTGCTCGCGGCGCGCTCTCTTGCCCATGAAG
 GTGGCCATTCGCGAGCTGGGCTGACCAAGGAGCGCCGACCAAGCTGTCTGTGGGCTGGAAGA
 TGGCAAGCTCATCTGCTGGTGTGCGGGGCGAGCCCTTGAGTGTGGCGAGCAGCAAGTCTGCGC
 GGAAGCTGTGGCGGTTCTCGCGGCACTCTCCAGGTGTGCTGGGAGAGCAGGAATACAAC
 CCTACTGAGGCGCGCTGAAGACTGGCAGTCCGGCTGCTCGGCGCGCGCCCGCCCGAGGCGCTG
 CGCCGGGAGAGCCCGCCCAAGAGTCCGCGGGAACACCCGGGGTGGGACGCCAGGGGGTGA
 CGGGGGCCCACTCTGCGGACCTCAGGGAATTTGGCGGGGATGTATCCCTCTCAGGAGATTTGGCG
 GCGGGAAGTCCGCGCCCTCGCGGCTGAGGGGCGCCCTCAGGGCGAGCACTGGCGTCT

FIGURE 23

MSQFEMDTYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRARLEGL
 RYTAVLKQQATQHSMAALLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVNP
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALETP
 MEAAELDEQREKLVLSAECQLTVVAVVPGLEVVTTQNVYFYDGSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSSPSQTTPRPQPGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFPWVLQDYVSPTLDLSNPAVFRDLSKPIGVVNPKHAQLVREKYESFEDPACTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDSDRQFHSVAAAWQARLESPADVKEIP
 EFFFYFPDFLENQNGFDLGCLQLTNEKVGDDVLPWASSPEDFIQHRQALESEYVSAHLHEW
 IDLIFGYKQRGPAEEALNVFYYCTYEGAVDLHDVTDERERKALEGIISNFGQTPCQLLKEP
 HPTRLSEAAEAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTQRLLSGPWPVPGSGVSGQALAVAPDGKLLFSGGHWDGSLRVLTALPRGKLL
 SQLSCHLDVVTCLALDTCGIYLSIGSRDTCMVWRLHQQGLSVGLAPKPVQVLYGHGAAVS
 CVAISTELDMAVSGSEDGTVIHTVRRGQFVAALRPLGATFPGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSYSLHLYSVNGKLRLASPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLDGLKLI VVVACQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTPEAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCCACCTTGTGAACCTCCTCGTGCCAGGGCTGATGTGCGTCTTCCAGGGCTACTCAT
 CCAAAGGCCATAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCCTGGGGCTCTTC
 TGGACCCTTAAC TGGGTACTGGCCCTGGGCCAATGCGTCTCGCTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCATTGGCATTGGAGCCCTCATCCTGACCCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGTGCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAAGGTGGTCTGCTCGGACAAAGTCACAGA
 CCTGCTGCTGTTCTTTGGGAAGCTGCTGGTGGTTCGGAGGCGTGGGGTTCCTGCTCTTCTTTT
 TTTTCTCCGGTCGCATCCCAGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCTATGTCTATCGCCAGCGGCTTCTTCAGCGT
 TTTGGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGGAAGAAGTGAAGCTCCGGCCCTGATCCAGGACTGC
 ACCCACCCCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAAGGTTT TAGGCCAGGCGCGTGGCTCACGCCGTGAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACTGAGTCAGGAGTTTCGAGACCAGCCTGGCCCAACATGGTGAACCTCC
 GTCTCTATTA AAAAATACAAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAAACAA
 AAAGATTTTATTAAAGATATTTTGTAACTC

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCVFQGYSSKGLIQRSVFNLQIYGVGLF
WTLNWVLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
NAFMLLMRNIVRVVLDKVTDLLFFGKLLVVGGVGLSFFFFSGRIPGLGKDFKSPHLNYY
WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKN
EAPPDNKKKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCGAGCGCCAGGCGCTCCGCCGCCGCT
GGCT**ATG**TTCGTGTCGATTTCGCCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCC
CAGTGTGACCACGTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAACTTGAAACTGC
ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAAACTGTGGAGCTAATGTAG
ACCTATTGGATATTCCTTCAACCTGATGAAGACACTATATCTTTGTGTGTGACTCCCATAGG
CCAGTCAATGTCTCAATGTATACACGATACCCAGATCAAATTACTCATTAAACAAGATGA
TGACCTTGAAGTTCGCCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
CAGGAAATGACAGTGATGGGTCCAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
GTGGAGCAAACCATGCGGAGGAGGCGACGGCGAGAGTGGGAGGCCCGGAGAAGAGACATCCT
CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
CAGTGGGTGCAAGACAAGATCACTCAAATGAAATAGGACTGATGTGTGGTCTCTGCAGCG
CCAGCTTTCCCGCCACAACCCGGAAGGAGGATGAGGAGAACAACACTCTCCGTGGACTGCA
CACGGATCTCCTTTGAGTATGACCTCCGCTGGTGCTCTACACAGCACTGGTCCCTCCATGAC
AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAGTTCC
AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAATGATTGAAGAGTCTGCAAATAAA
TTTGGGATGAAGGACATGCGCGTGCAGACTTTTACGACTTCATTTTGGGTTCAAGCACAAGTT
TCTGGCCAGCGAGCTGGTCTTTGCCACCATTGTCTTTGATGGAGAGCCCGAGAAGGATGGCT
CAGGGACAGATCACTTTCATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
TACCATGGCCTGGAATCTGCCAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTGCCAGCTGC
CTTTGCACCAACCTCGTCATCTCCAGGGGCCCTTTCTGTACTGCTCTCATGGAGGGCAC
TCCAGATGTCATGCTGTTCTCTAGGCCGCGATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
AGTCCCTTGTGTGTTTCGACAAAGAACCAGCGCTGCAAACCTGCTGCCCTGGTGATGGCTGCC
CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCAGCAGCTC
GGACAGGAAGAACTTTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
TGCTGCACAACCATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
CTGAGCAACTTATTTCCCTCCTGTCC**TAG**GAATTTGATTCCTCCAGAATGACCTTCTTATT
TAGGTAACCTGGCTTTCATTTAGATTGAAGTTATGGACATGATTTGAGATGTAGAAGCCATT
TTTTATTAATAAAATGCTTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVEDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
LEHKEQFHYFILINCGANVDLLDILQPDEDTIFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
LEVPAYEDIFRDEEEDEEHSGNDS DGSEPSEKTRLEEEIVEQTMRRRQRREWEARRRDILF
DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH
VSRHNHRNEDEENTLSVDCTRISFEYDLRLVLYQHWSLHDSLNTSYTAARFKLWSVHGQKR
LQEF LADMGLPLKQVKQKQAMDISLKENLREMIIEESANKFGMKDMRVQTF SIHFGFKHKFL
ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSNLDKLYHGLELAKKQLRATQQTIASCL
CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
LSMEHGTVTVVGIPPETDSSDRKNFFGRAFEKAAESTSSRMLNHHFDLSVIELKAEDRSKFL
DALISLLS

FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCCGCGTGGCTATGNTCGTGTCGATTCCGCA
AAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCTTCTCTTCGTGGCCTCGGANGTGGAT
GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
GGTTCAGTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
ATTATTTTATTCTATAAAGTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
CGATACCC

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CGAGAACCCCTCTCTTTGGGCTCTGGATTGGGAGCCCTTTCCAGTACCATTTTTTCTAGTGAAC
CAGGAGGGACGCTATGACAGAAACACCTCAACCCAAAGGAATAGACTACAGGCCCAATTG
GCTGACTATTGGCTATAGAAAAAGGAAGACGAAAGACAGACTTTTTTTTGGAAAGCTAA
STCTTCCCTTTATCAGGTCAGAAACCCCCCTTCTGGAGTATTTACAGCTTTTTAAACATT
GAGTAAAGTACGCTCCGGTCAACC**ATG**CTGACAGCGCCCTGGTCCCTCTTGCTGGGACGGCTC
TGCTCTTTCTCCTGCTGTGTGAGTCCGTATGTGGAGCTCACTTTGACAGAGCTGTGGC
CAGCGGCTGCAACGGTGTGTGATCTTGAGGACCCCTGGATCTGCCCAAGTATCTCTAGC
CTCTTCTCTCGGGCCGCCCCACGCCCTGCTGGAGTCAGACCTACATTAATATACCAT
CTGAAGGGTGACAAAGGGGACCGAGCCCAATTGGGACTGCCAGGGTACATGGGCGAGGGG
TCCCAGAGGGGACCTGGCCCTCAGGCGCAGCAAGGGTGACAAAGGGGAGATGGGCGAGCCCG
GCGCGCTGCTGACGAAGCGCTTTTTCGCTTCTCAGTGGGCGCAAGGACGCCCTCTGCACAGC
GCGAGGACTTTGAGATCTGCTTTCTGAAAGGGCTCTTTGTGAACTTTGATGGGTGCTTTGA
CATGCGCCCGGCGAGGTTGTCTGTCTCCCTGGCTGGCATCTCTTTCAGCTCAATGTGTG
ACACTTGGAAATGACGAGAGCTACGTGCACATTATGCAATACAGAAAGAGGCTGTGATCA
CTGTACGCGCAGCGCTGACGCGCAGCATCATCAGAGCGCAGGTGTGATGCTGGACCTGGC
CTACGGGGACCCGCTTGGGGTGGCGCTCTTCAAGCGCCAGCGCGGAAGGCCATCTCAGCA
ACGACTTTCAGACCTACATCACTTTCAGCGGCCACCTCATCAAGCGCGAGGACGACT**TGA**GGG
CCTCTGGGCGACCTCCCGCTGGAGAGCTCAGGTGTGGTCCGCTGCCCTCTCGAGGGCTCAG
TTTTCACCTCTGGAAGCAGGAGGCGAGGAGGCTCCCGGGGACCTGGCATCTTGGGGAGA
CCCTGCTCTCTCTTCTGCTGCTGATCATCTCCAGCCATTTTCTGCTCTCTCTCTCTCT
TGGACCTATTTTAAAGAGCTCTGAACCTAAATATTCTAGAATTTCCGAGCGCTCGATGGC
AGCACTTCTCAAATCGGAATGCTATCGGAATCCAGCGGGGTTCGTGTAAATGAGATTTCT
GACTCAGCAGCTGTATGGTGGTTCAGGATCTGTGTTTCTCATATGTCTCGGGTGATGCT
ATGGGGTCACTGTAGTGGTCACTCAGGACCAACAGGTTCTAGGACTTCTCAATATCTCA
TACTTTCTCAACATCTTGGAAATCTCTCAATCTCTAGAAATCTCCCAACATTTTTTTCT
TGAGACAGACTTTGCTCTGTGTGGCCAGCTAGAGCGAGCTGTGCAATCTCAGTTTCACTGC
AACCCTTGCTCCCGGTTTCAAGCGATTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
AGGCGCTCTACCATGCTTGCTAAATTTTGTATTTTGTAGAGAGTGGGGTCTGACCAT
TTGGCCAGGCTGCTGTGAATCTCTGACTTCAGGTAGCCACCGGCTCTCTCTCTCTAAAT
TTGTGGGATTACAGGTGTGAGCCACGCTGCCGTGCCAAATCCAACTTCTTAATTTCTCT
CTCTCCAGGGGCTCCCGTGCTATGTTCTCTTTACCCCTTCCCTCTCTCTCTGCTCAGGC
TGACCACTCTCAGCCACCGTTCATTATTTCATTATTAACACTGAGCACTCACTGTGTCT
GGGTCCCGGGGAGGGGTGAGGGGTGACAGACGCCCTGCCCTGCCCTCAGTGAATGGCCA
GTCCAGCCAGGCGGGGAGAGTGTTCATACAGTTTAAAGCAGACCCAGAGCTCATGGG
GCTGTGTGTTCTGGGTGTTCAAGTGTCTGTGTCTCTCCATTACCACTGTCTCCCAAGCTGG
TGGACGGGGTCCCGGTGGCAGGGGACGATCTCTCTCCGTTCTCATCACTGCCAC
TGCTCATGTGTACAGCAAAACCCAGGGGGCTTGGCCAGTCAAGGGTTCTGTGAGGAGAGG
ACCCAGGAGTGTGGGGGCATTTGGGGGGTGAAGTGCCCCGAAGAAATGCAACCAACACCCA
TAGCTCTCCCCAGGAGTATACGGCATCTCGCAGAGAACCTGCCCTCTCATCTGGGATCCC
CTTCTGCTCTCTCCAGGGTCTGCGAGGGCCCTGTCTCAGTCTCTTCCACCAAACTCATCT
GAATCTCGTTTCCCCAGGGGCTCAGCTGCCCTCAGACACTGATGTCTGTGCCCGAGGTGCT
CTCTGCCCTCATGCCCCCTCACCAGGCCCACTGCCCCAGTCTCCAGGCTTTATCAAGGTG
CTAAGGCCCGGGTGGGCGAGCTCTCTGCTCTCAGAGCCCTCTCCGCGCTGGTGTGTCGTTTAC
AAACACCTTGACGAGGAGGCGACCGGAAGGCCCGAGGTTTAGAGCCTCAGCAGCTTGGGG
AGCTAGAGCAAAAGGAGGACCTCAGGCCCTCCGTTTCTTCTCCAGGGTGGGGTGGGCTGGT
GTTCCCTTAGCCTTCAAAACCAAGTGGGCTGGCTTCTTCCCGAGAGGAGGCGGCTCCGC
CCATTGTGCTCATCAGACTCTGGGGCTGAGGTGCGCCCGGGGGTGATCTCTGTGCTCAC
AGCGAGGGAGGCGCTGCTCATGCGGATGACGCGAAACAGGGTTGACCAAGTGCAGGA
AGACTGTGCTCATTAACCAACCCGCTGCTGATCTCGCCCTGCTGACCCCGCACCGCTGCC
GTCCAGCATGATTAAAGAAATGCTGCTCTCTCTTGGAAAGGAAAAA

FIGURE 30

MVTAALGPVWAALLLLFLLMCEIRMVELTFDRAVASGCQRCCDSEDPLDPAHVSSASSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPGQEPGPQGSKGDKGEMGSPGAPCQKR
FAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPSERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:**Signal peptide:**

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTGTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAGACTG
 AGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCCGCCGCCCTCCCGGGACAGAAGATGTG
 CTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCTTGGGGTGCAGG
 GCTGCCACTCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCAGCTGCCCGCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAGCTCTTTGAGAACGGCAT
 CACCATGCTCGACGCAGACGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTCAC
 AGAACAGATCGCCAGCCTGCCAGCGGGGTCTCCAGCCACTCGCCAACCTCAGCAACCTG
 GACCTGACGGCCAACAGGCTGCATGAAATCACCATGAGACCTTCCGTGGCCTGCGGCGCTG
 CGAGCGCCTTACCTGGGCAAGAACCCGATCCGCCACATCCAGCCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCGCTGCGC
 CTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGCAT
 CCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTACGCGCTTTCGCGAACCTCCACGACCTGGATGTGTCCGACAAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGCTCCGGGCTGACGCGCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCGGAGGACCTGGCCGGCTGGCTGCCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCGCTGCCTGGGCACTCTCGGGCTCTTCCCGCGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTGAGCTGGTTGGCCCTG
 GGTGCGCGAGAGCCAGTCAACCTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCAGCCACCAAC
 ACCACAGCCACAGTGGCCACACAGGCGCCGTGGTGGCGGAGCCACAGCCTTGCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGCCACTGAGGCCCCAGCCCGCTTCCA
 CTGCCCCACCGACTGTAGGCGCTGTCCCCAGCCAGGACTGCCACCCTCCACCTGCCTC
 AATGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGGCCCCAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACAGTCA
 CGCCGAGGCCACACAGGTCCCTGACCTGGGCATCGAGCGGTGAGCCCTCCCTCGCTGCG
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTACCTA
 TCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCACCCAGCTGCGGCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGG
 CCCGGGCGGCTGCCGAGGGCAGGAGGCGCTGCGGGGAGGCCATACACCCACAGGCTGCCA
 CTCCAACCCAGCCCGAGTCAACCCAGGCCCGGAGGGCAACCTGCCGCTCCTCATGTGCGCCG
 CCCTGGCCGCGGTGCTCCTGGCCGCGCTGGCTGCGGTGGGGGACGCTACTGTGTGCGGCGG
 GGGCGGGCCATGGCAGCAGCGGCTCAGGACAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAACCTGGAGGAGTGAAGGTCCCTTTGGAGCCAGGCCGAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGCTGTAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTTGGCCTC
 CAGTCAACCCTCCACGCAAGCCATACATTAAGCCAGAGAGACAGGGCAGCTGGGGCCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCCCTCTGCTGCCACACACGTAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGGCTGTTCCTCTGGA
 CCTCGGTCTCTGTGATGTGCTGTGGCCAGCTGACGAGCCCTAAGCTCCCCAGAAC
 CGAGTGCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGGCCTGCCATGTGCTGTTAACGCATGCCTGGGTCCTGCTGGGCTCTCCCACTCCAGCGGCA
 CCTTGGGGCGAGTGAAGGAAGCTCCCGGAAAGCAGAGGGGAGGCGGTGAGGCGGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATATATAAGAGATCCTTTCCCATTTATTCTG
 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGAAGACAACAGATGATAG
 AAGGCTTTTTGTAAGAAAAATAAAGATGAAGTGTGAA

FIGURE 32

MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVECTARQGTTPRDPVPPDTVGLYVFEN
GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
GILDTANVEALRLAGLGLQQLDEGLFSRLRNLHDLVDSDNQLERVPPVIRGLRGLTRLRLAG
NTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCLSWFG
PWVRESHVTLASPEETRCHFFPKNAGRLLLELDYADFGCPATTTTATVPVTRPVVREPTALS
SSLAPTWLSPTAPATEAPSPPTAPPTVGPVPQPDCCPPSTCLNGGTCHLGRHHLACLCPE
GFTGLYCESQMGQGTSPPTPVTPRPPRSLTLGIEPVSPSLRVGLQRYLQGSVVQLRSLRL
TYRNLSPGDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPPLGPRVPEGEEACGEAHTPPA
VHSNHAPVTQAREGNPLLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGVGPGAG
PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGLQSPHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCATATGAGGAAATAGTGGTAAAAATCCTTGGAAATACAAATGAGACTCATCAG
 AACAATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTGTAGCTCCAGAGCTGCCAG
 AAGAAAGGGAATGATGACCACTGCTCCAACATGCTCTAAGAAAGGTTCCCGAGACTTG
 ACCCGAGCCACCAACGACACTGGATTTATCCTATAACCTCCTTTTCAACTCCAGAGTTCAGA
 TTTTTCATCTGTCTCAAACTGAGAGTTTGTGATGCTATGCCATACAGAAATCAACAGCTGG
 ATCTCAAAACCTTTGAATTCACAAAGGAGTTAAGATATTTAGATTGTTCTATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCTCAGGTATTTAGATCTTTCTTTTAACTGACTT
 TGACACCATGCCATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCTTAGGTTTGA
 GTGGGGCAAAAAACAAAAATCAGATTCCAGAAAAATGCTCATCTGCATCTAAATATCTGTC
 TTCTTAGGATTGAGAACTTCTCCTATTATGAAGAAGGTAGCCTGCCATCTTAAACACAAC
 AAAACTGCACATTTGTTTTACCAATGGACACAAATTTCTGGGTTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
 ATGCAACGAAATCTTAGTTTAGAAAAATGCTAAGACATCGGTCTATTGCTTAATAAGTTGA
 TTTACTCTGGGACGACCTTTTCTTATCTTACAATTTGTTGGCATACATCAGTGGAACT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGTGACTAC
 TCAAAATCTGTAATGGAACATATAAATTTGGAGCATGTACATTTAGAGTGTTTTACATTCA
 ACAGAGATAAAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGACAATATCAATG
 CACAAATGGCCACACATGCTTTTCCGAATTTATCCTACGAAATTTCAATTTTAAATTTTGGC
 AATAAATATCTTAAACAGACGAGTTGTTTAAAAGAACTATCCAATCGCTCAGTTGAAAACCTCT
 CATTTTGAATGGCAATAAAGTCGAGACACTTTCTTAGTAGTGTCTTGTGTAACCAACAC
 CCTTGGAAACATCTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAAATGCTCA
 TGCCAGAAAACCTGGGTCAATGAACTGTGCATACAATAAATTTGCTGATCTGTCTCAG
 GTGCTTGCCCAAAATGATTCAAATACTTGACCTAAATAAACAACAAATCAAACCTGTACTTA
 AAGAGACTATTAATCTGATGGCCTTACGAGAATCAAAATTTGCAATTTAAATTTCTAACTGAT
 CTCCTGGATCTGAGTCATTTTCACTAGACTTTCAGTTCTGAACTGAAATGAACTCTATTCT
 CAGCCCATCTGCGATTTTGTTCAGAGCTGCCAGGAAGTTAAACTCTAAATGCGGGAGAA
 ATCCATTCCGGTGTACCTGTGAATAAAAAATTTTATTGAGCTTGAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTCATACACCTGTGAATACCCCTTAAACCTAAGGGGAACATG
 GTTAAAAGACCTTTCATCTCCACGAATTAATCTTGCAACACAGCTCTGTGTGATGTACCAATG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCCTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAAACATGGCACAGGGTTAGGAAAAACAACCA
 AGAACAACTCAAGAGAAATGTCCGATTCCACGCAATTTATTTCATACAGATGAACATGATTTCT
 TGTGGGTGAAGAATGAATGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTGCG
 CTTTATGAAAGCTCATTTGACCTGGCAAAAGCATTAGTGAAATATTGTAAGCTTCTATGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAAATGAGTGGTGCCATT
 ATGAATTTCTACTTTTGGCCACCACAATCTCTCCATGAAAATTTCTGATCATATAAATCTTATC
 TTAATGGAACCCATTTCCATTTCTATTGCAATCCCCACAGGTATCATAACTGAAAGCTCTCTC
 GAGAAAAAAGCATACTTTGGAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGCCAA
 ACCCTCTCAGCTGCTATTAATGTAAATGATATAGCCACAGAGAAATGATGAACTGCAGACA
 TTCACAGAGTTAAATGAAGAGTCTCGAGGTTCTACAATCTCTCTGATGAGAACAGATTGTCT
 ATAAATCCCAAGTCTCTTGGGAAGTTGGGGACCACATACACTGTTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGCAAAATTTTATAAATAAAAAATGGTTATTTCCCTCATATA
 TCGATTTCTAGAAGGATTTCTAAGAATGATCTTATAGAAAACCTTTACAAGTTTATAAGG
 GCTTTATGAAAAAAGGTGTTCTATCCCAAGGATTTTATAATCAATGAAATGTGGCCAGGTGCG
 AGTGGCTCAGCTTTGTAATCCAGCACTATGGGAGGCCAAGGTGGGTGAGCCACAGAGGTCAA
 GAGATGAGACCACTCTGGCCAAACATGGTGAAACCCCTGTCTCACTAAAAATCAAAAAATTA
 GCTGGGGGATGTTGGTGACGCGCTGTAGTCCAGCTACTTTGGGAGGCTGAGGCGAGGAAATCG
 CTGGAACCCGGGAGGTGGCAGTTGCAGTGAGCTGAGATCGAGCCACTGCACTCAGCTGATGCT
 GACAGAGCGGAGCTCCATCTCAAAAAAAGAAAAAAGAAAAAATGAAAAATCAATCC
 TCATGGCCCAAAAATAGGCTTAATTCATAAATATATAGTACATTAATGTAAATATAATATTA
 GCTGCCACTAAAAAGAATAAGGTAGCTGTATATTTCTGGTATGAAAAACATATTAATAT
 GTTATAAATCTTAGGTTGGTGCAAACTAAATTTGGTTTGGCATTTAAATGGCATTTGAA
 ATAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTGGGCTGGGAGGTGGA
 TTACAGGAGCATTTGATTTCTATGTTGTATTTCTATAATGTTTGAATGTTTGAATGATGA
 ATCTGTATTTCTTTTATAAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLTPATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTLPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDLFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLTKMDIENLTISNAQMPHMLFPNYPTKFQYLNFANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENCSPETVVNMNLSYNKLS
DSVFRCLPKSIQILDNLNNQIQTVPKETIHLMALRELNIAFNFLTDLPGCSHFSRSLSVLNE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKDVHLHELSCNTALLIVTIVVIMLVGLAVAFCCCLHFDLPWYLRMLGQCTQTWHRV
RKTTQEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLSPNFVQNEWCHYEYFAHHNLFHENS DHIILILEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

GGGGGCTTTCTGGGCTTGGCTGCTTGAACACCTGCCTCCAAGGACCGGCTCGGAGGGGTGCGCGGGAAGG
 GAGGGAAGAAAGAGGGCGGGGCGGCCCCCTGCGGCCCGCCCGCGCTCTGCGCGCCCTGTGCGCGCCGCGC
 CGAGCCAGCCAGCCCGCGGGCGGTCACAGCGCGAGCCGCGCGCTCCCGCGCCAGCGCGCGCTGCT
 CTGCTGTGCCCTGCGCCCTTGCCCGCGCCAGCTTCTGCGCCCGAGCCGCGCCCGCGCCCGCGGTGACCGTGA
 CCTGCCCTGGGCGGGGCGGAGCAGGCTATGCTCCGCGCGGGGACCGCTACAGCGCTGCGCGCTGCTC
 CTGGCAGTGACCTTGCCCGGGTGGAGGCCAGGCGCGACCTCGAGGACCTGATTTATACGGGAGGAGAT
 CTGAGCCCGGAGCCCTACTACGCGCGCCGAGGCGCGAGCTCGAGACCTTCTCTCGCCGCTGCTGCGGGGCG
 CCGGGAGGAGTGGGAGCGGCCCGCAGGAGCCAGCGCCGCCAAGAGGGCCCAAGCCGACCAAGCTCCC
 AAGAGGGAGAGTGGCTCGCGCGCGGCTCCACAGCTAAACACAGCAAAAGTTATGAGAACCAAG
 CTCTGAGAGGCTGCCACAGTATCAGCTGTCCGTGTGGCCGCTGAAGATGTGAGAGAGAGTGGCCCACTC
 TTGGTCTGGAACCTTAAAAATCACAGACTCCAGCTCCATGCCCTCCAGGTGAAGCGCTATGCGCTGGGGGCA
 CATCGAGGGAGACTCAACATCCAGCGGGCATTAAATGAAATGATTTTATGACGCGAGCGTGGTGGCGGGGAAG
 AATGACCTCCAGCAGTGGATTGAATGGATGCTCGGCGCTGACCAGATTCACTGGTGATCACTCAAGGGA
 GGAATCCCTCTGGCTGAGTGACTGGGTGACATCTATAAGGTCACTGGTGAAGCAATGACAGCCACAGCTGGT
 ACTGTTAAGATGATCTGGAGACATGATATTGAGGGAACAGTGAAGAGGAGATCCCTGTTCTCAATGAGT
 ACCCGTCCCATGGTGGCCCGCTACATCCGATAAACCTCAGCTGCTGTTTGATAATGGAGACATCTGCATGA
 GAATGGAAGTCTGGGCTGCCCATCGGACCTCTAATAATTATTAACCGCGGGAAGAGATGACCACTACT
 GTAGCCTGGATTAAAGCACCAATTATAAGAAATGGCGCAGTTGATGAAAGTTGTAATGAAATGTTGCC
 CAATATCACCAGAAATTAACAATTGAAAAAGCCAGGGGCTGAAGCTGTATGCTGTGAGATCTCAGATC
 ACCCTGGGAGCATGAAGTGGGTGAGCCGAGTTCCACTACATCGCGGGGGCCACCGCAATGAGGTGCTGGCG
 CGGAGGTGCTGCTGCTGCTGGTCAAGTTCGTGTGAGGACTACTTGGCCGGAATGCGCGCATCTGCCACT
 GGTGGAGAGACCGCGATTCACTGCTCCCTCCCTCAACCCGATGGCTACGAGAGGCCCTACGAAGGGGCGCT
 CGGAGCTGGGAGGCTGCTCCCTGGGAGCGTGGACCCAGATGGAATTGACATCAACAACAACTTCTGATTATA
 AACACGCTGCTCTGGGAGCGAGGATCGACAGAAATGTCCCAAGGAAAGTCCCAATCACTATTGCAATCCC
 TGAGTGGTTCTCTCGGAAAAATGCCAGGTGGTGGCCGAGACAGAGCAGTCAATGACCTGGATGGAAAAATCCC
 CTTTGTGCTGGGCGCAACTCGAGGGCGCGAGCTGGTGGTGGCGTATCCCTACGACTGGTGGCGTCCCC
 TGGAGAGCGAGGAACACACCCCAACCCCGATGACCACGTGTCCGTGGCTGGCCTACTCTTATGCTCCAC
 ACACCGCTCATGACAGACGCCCGAGGAGGGTGTGCCACAGGAGGACTTCCAGAGGAGGAGGGCACTGTCA
 ATGGGCTCTCTGGCACCGTCTGCTGGAAGTCTGAACGATTTCACTACCTTATACAACTGCTTCGAATG
 TCCATCTAGCTGGCTGTGATAAATACCCACATGAGAGCCAGCTGCCGAGGAGTGGGAGATAACCGGGAATC
 TCTGATCTGTGTCATGGAGCAGTTTATCGTGGCATTAAAGGCTTGGTGAAGATTCATCTGGAAGGAATCC
 CAAACGCCATTATCTCCGTAGAAGGCATTAAACATGACATCGGAACAGCAAGTGGGATTACTGGCGCTC
 CTGAACCTGGAGATATGTGTCACAGCAAGGCGCAAGGTTTCACTGCACTCCACAGAACTGTATGTTGG
 CTATGACATGGGGGCCCAAGGTGTGACTTCACACTTAGCAAAACCAACATGGCGAGGATCCGAGATATCC
 AGAAGTTTGGGAAGCGCCCTGACCTGCCAGCCAGGCGGCTGAAGCTGCGGGGCGGGAAGGACGACCAAGT
 GGGTGAACCTCCCTGGGCTTGAAGTCTGTGGGACCATGCAAAATTAACCAATGCTAGTGTGACTCATG
 TGGACTCACTCACTGTTGTTCTCTGTAATTCAAGAAGTGCCCTGGAAGAGAGGCTGCAATGTGAGCGAGTCC
 CAAAGGGAAGGCTGGAGCTGGGCTGTTTCTTTCTTTGTTCCGATTCTTCAAAATTAACCTTGGACAGCA
 CGAGAGAAAGCTGTGAGGATGAGAGAACTCAGCAAGCCAACTGGGAATCAGAGAGAGAGGAAGGAGGG
 GAGCTCTTCCCTTCAGAGCCTCTGGCTGCATAGAAAAGATCTTGGTCTTCCCTGTTTGGCTGGCAGG
 GTTCCAGCTGCATTGCAATTTCACAGCTAAATTCGACATTTCCCGAGCTGGCGTGTCCCAATGTTACCA
 TTTGAGATGCTCCAGCGCTTCCAGAGAACTCCACCTCTCTGGCCCTGGGACATTCGAACTGCTTGAATCTGTT
 ATTCTGCTCTCTTTGACAAATAGCGTCAATGCCAAGTGACATCACTGAGCCTCTGTAATCTGTTTGTCTCT
 TTTTCAACAAGGAGTGTGTCAGAAAAGGAGAGAGGCTGAGATCTTACAGGATTTTGGGAGCGCAAGCA
 TGGAGCTTCTTGCAGAAATCTGGGTCCAGCCTTCTGAGGGCCAGAAAATTTAGCCTGGATCTCTCTTTTAC
 CCCAGTATAGGAGAGCGAGGCTGCCAGCTTCTGAGGGCCAGAAAATTTAGCCTGGATCTCTCTTTTAC
 TTTGAGATGCTCCAGCGCTTCCAGAGAACTCCACCTCTCTGGCCCTGGGACATTCGAACTGCTTGAATCTGTT
 GAAATTCAGTCTCATGGGTGGCCCTATATCAGCCTGGGAGTTATTTTGATATGAGAAATGCGACATCTTCCA
 GATTAGGCTAAATGTAATGAAAACCTCTTAGGATTATCTGTGAGCATGCTTTGGGAAGAAATTTTGAATTA
 CTTCGCAAGAAAAAGATGTCCTCACTTTTGTAAATGTGCTGCTCATTGACCTGGGAAAAATGAAAAAAA
 AATAAAGCAATGGTAAGCCCTTAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPPYARPEPELETFSPLP
AGPGEEWERRPQEP RPPK RATKPKKAPKREKSAPEPPP GKHSNKKVMRTKSSEKAANDHDS
VRVAREDVRESC PPLGLETLKITDFQLHASTVKRYGLGAHRGLRLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRRLRFTGVTIQGRNSLWLSDWVTSYKVMVSNDSHTWTVKNGSGDMIF
EGNSEKEI PVLNBLPVMVARYIRINPQSWFDNGSICMRMEILGCPLDPNNYYHRNEMTT
TDDLDFKHHNYKEMRQLMKVVNEMCPNITRIYNI GKSHQGLKLYAVEISDH PGEHEVGEPEF
HYIAGAHGNEVLGREL LLLLVQFVCQEYLARNARIVHLVEETRIHVLPSLNPDGYEKAYEGG
SELGGWSLGRWTHDGDIDNNNFPDLNTLLWEAEDRQNVPRKVPNHYIAIPEWFLSENATVAA
ETRAVIAWMEKIPFVLGGNLQGGELVVAYPYDLVRS PWKTQEHTPTPDDHVFRWLAYSAST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEVWTNNAESLIVFMEQVHRGIKGLVRDSHGKIPNAIISVEGINHDIRTANDGDYWRLL
NPGEYVWAKAGIEFTASTKNCMVGYDMGATRCDFTL SKTNMARI REIMEKFGKQPVSLPARR
LKLGRKRKRORG

[illegible]

MRPGLSFLALLFLFLGQAAGDLGDVGPPPIPSPGFSSFPGVDSSSSFSSSSSSGSSSSSRSLGS
GGSVSQLFNFTGSGVDDRGTCQCSVSLPDTTFPVDRVERLEFTHAVLSQKFEKELSKVREYV
QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
LEVEIRNMTLLVEKLETLDKNNVLAIRREIVAKTKIKECEASKDQNTFVHPPPTPGSCGH
GGVVNISKPSVVQLNWRGFSYLYGAWGRDYSQPHENKGLYWVAPLNTDGRLLLEYRYLYNTLD
DLLLYINARELRITYQGSGTAVYNNMNYVMYNTGNIARVNLTNTNTIAVTQTLPAAYNNR
FSYANVWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
MVCGVLYATRMNTREEIFYFYDDTNTGKEGKLDIVMHMKQEKVQSINYNPFDQKLYVYNDG
YLLNYDLSLQKPTO

FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC

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FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCAGAAAGAAGCTGTCTCCATCTTGCTGTAT
 CCGCTGCTCTTTGTGACGTTTGTGGAGATGGGGAGCGTCCTGGGGCTGTGCTCCATGGCGAGCT
 GGATACCATGTTTGTGTGGAAAGTCCCCGCTGTTTGTCTATGCCATGCTGTCCATAGTGGAAAC
 AACTCCACCTGTAACATAGATTGATCTATGCACCTTTCTTGCTTTGGAGTATGTGTAGCTTG
 TGTAAATGTTGATACCGGAATGGAAGAACAACCTGAATAAGATTCTCGGATTTGTGAGAAATG
 AGAAAGGTTGTGCCCTTGTAAACATTTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GTTATTGGCTATGTTCTATCTTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGCAATTA
 TTATTGGGCGATTCTTCATCCAGAAGGAACCTTTACAACCTGTGTGGTTTTATGTAGGCATG
 GCAGGTGCCCTTTTGTTCATCCTCATACAACCTAGTCTTACTTATGATTTTGCACATTCATG
 GAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACCTCGAGATGTTGGTATGCAGCCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGTCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTCAAGAAACAGGCGTTTATCAGTGTCAACATGCTCCTCTG
 CGTTGGTGCTTCTGTAATGTCTATACTGCCAAAAATCCAAGAATCACAAACCAGATCTGGTT
 TGTATACAGTCTTCAGTAATTACAGTCTACACAAATGTAATTTGACATGGTCAGCTATGACCAAT
 GAACCAGAAACAAATTGCAACCCAGTCTACTAAGCATAAATGGCTACAATACAACAGCAGC
 TGTCCCAAGGAAGGGCAGTCAGTCCAGTGGTGGCATGCTCAAGGAATTAAGGACTAATTC
 TCTTTTGTGTGTGATTTTATTCAGCATCCGTACTTCAAAACAAATAGTCAGGTTAATAAA
 CTGACTCTAACAAAGTGTAGATCTACATTAATGAAGATGGTGGAGTGAAGATGATGGATG
 ACTGGAGGATGGGACGATGTTCCACGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GTTATTCCTTCTTCTTCACTTATGCTTTTCTGGCTTCACTTTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTTCCAGTTGGATTGGCATCGTGTATGTTTGGACAGTCCGAGGACAGCTTGTCT
 TTACAAATCGTGAATTTGACTGAGTGTGAGACTTCTAGCATGAAAGTCCCATTGATTTATGC
 TTATTGAAACAGTATCCCAACTTTTGTAAAGTTGTGTATGTTTGTCTTCCCATGTAAC
 TTCTCCAGTGTTCTGGCATGAATTAGATTTTACTGCTTGTCAATTTGTATTTTCTTACCAA
 GTGCATTGATATGTGAAGTAGAATGAATTGCAGAGGAAAGTTTATGAATATGGTATGAGT
 TAGTAAAAGTGGCCATTATTTGGGCTTATCTCTGCTCTATAGTTGTGAAATGAAGAGTAAAA
 ACAAAATTTGTTGACTATTTTAAAATTATATTAGACCTTAAGCTGTTTATGACAAGCATTA
 GCAAAATGTATGGCTGCCCTTTGAAATATTTGATGTGTGGCTGGCAGGATACCTGCAAGAAC
 ATGGTTTATTTTAAAAATTTATAACAAGTCACTTAAATGCCAGTTGTCTGAAAAATCTTATA
 AGGTTTTACCCTTGATACGGAATTTACACAGGTAGGAGGTGTTTAGTGGACAATAGTGTAGG
 TTATGGATGGAGGTGTCGGTACTAAATTTGAATAACAGGTAAATAACTTACTTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTGTTTGGTTGTTTTAAACTCATGAAGTATGGGTTCAGT
 GGAATGTTTGAACCTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAATCATGGGTAGAGA
 AGGAAGTGTGTTGAAAGTCACTTTGAAAGTTAGTTTTGGGCCAGCAGGCTAGCTCACCTTT
 GGTAAATCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAGCCAGGAATTCAGACCA
 GCTTGGGCACATGGTGAACCTGTTCTATAAAAAATAATCTGGCTTTGAGCATATGCTCTGGTGC
 CAGCACTGAGAGGCTAGTGAAGATTGCTGAGCCCCAGGCAAAAGTTGCAGTGAGCAAGTCA
 CGTCACTGCACCTCTAGCTGGCAGCAGAGTAAGCCAAAAAATATATATATTTGAAATCAAGG
 AGGCCAAAATTTGACAGGGAAGGAAGTAACTGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAATCTTAGTCCAGTTCTCTCATTTAAAAAATGAAGACACTGAAATACAGACTTAAATA
 GCTCAGATAGCTAATTTAGGAAATTTCAAGTTGGCCAATATAGCATCTCTCTGCATCTTAA
 AATTAATTTCTATTCAAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
 GAGTGGATTGCTGGTGTCCAGCATGACCCATAAACAGGTGAGAAGAAATGATGAAATGTTTT
 AGAATAAACTCTGCTTATAGTATACTACACAGTTCAAAGATGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTTGAAATATATAGATTATGTAACCTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTAGTTATTTGATGTGTCACTAGTGCTTAATGAGCTTTTAAATCTCAACT
 TCTCTTTTAAATAATTTTAAATGTAATGTGAATGGAATAAACAATTCAGCTTAAATCCCCAAC
 TTATCTCTGTGTAGACATTGATTTCCACAATTTGAAATGGCTGTGTTTTACCTCTAAATAA
 ATGAAATTCAGAGAAAAAATAAAAA

MGSVLGLCSMASWI PCLCGSAPCLLCRCPCSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVPNCNILVGKAVYRLCFLGLAMPYLLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFVYVGMAGAFCPILIQVLVIDFAHSWNESWVEKM
EEGNSRCWYAALSLATALNYLLSLVAIVLFFVYTHPASCSENKAFISVNMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCFYSSIRTSNNSQVKNLTLSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYSFHFMLFLASLIIMTTLNWSRYEPSREMKSQWTA VVVKISSSWIGI
VLYVWTLTVAPIVLNTRNDF

CGCAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTGCTATGCCGATGCTGTCCTAGTGAAACAANTCCA CTGTAAC TAGATTGATCTA
TGCACTTTTCTTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCGGAATGGAAG
AACAACTGAATAAGATTCTCGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAAACATT
TTGGTTGGCTATAAAGCTGTATACGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAGATGAAGATGCACTGATCTTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTTGCTCGACGAATTGCAATTATATTGGGGC

FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

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AAGAAGCTGTCTCCAICTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATTGTTTGTGTGAAGTGCCCCGTGTT
TGCTATGCCGATGCTGTCTAGTGGAACAACTCCACTGTAAC TAGATTGATCTATGCACCTT
TTC TTGCTTGTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAACAACCT
GAATAAGATTCCTGGATTTTGTGAGAATGAGAAAGTGTTGTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTTTTA
CTAATGACCTCAAGTAGAAGATGCAGTGCATCTTAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTTGCTGCAGCAATTGCAATTATTATGGGGC

FIGURE 45

GCTGTCCTTAGTGGAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCCTTG
CTTGTTGGAGTATGTGTAGCTTTGTGTAATGTTGTTCCCGAGGATTGGANGAACAACTGAATA
AGATTCCCTGGATTTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACAATTTTTGGTTGGC
TATAAAGCTGTATATCGTTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATTCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACTAGT
CTTACTTATTGATTTTGCACATTATGGAATGAATCGTGGGTTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTTCAGAAAACAAGGC
GTTTCATCAGTGTCAACATGCTCCTCTGCGTTGGTGCTTCTGTAATG

FIGURE 46

CTCGGGCGCGACAGGCAGCTCGGTTTGCCCTGCGATTGAGCTGCGGGTCGCGGGCGCGGCCCGCTCTCCAAT
GGCAAAATGTGTGGCTGGAGGCGAGCGGAGGCTTTTCGGCAAAGGCAGTCAAGTGTGTCAGACACCGGGGCGAG
TCTGTGGAAGCAGATAAAGAAACATTTATTAACGTGTCTATACAGGGGAGCGCCCGCGGGGCTGTGCG
ACTCCCCCGGGAACATTTGGCTCCCTCCAGCTCCGAGAGAGGAGAGAAGAAAGCGGAAAGAGCGAGATTAC
GTGGTTTCCAGCCAAATGGACCTGATCGATGGCCCTCTGAATTTATCAGATATTTGATTTATTAGCGATGCC
CCCTGGTTGTGTGTTACACGACACACCTGACACAGGCTCTGGCTCGCTTCCCTCCCTGTTTCCAGCTCC
TGGGCAATTCACCATCTGTTTTCACACTCTCCGCCGAGGGGAGCAGGAGCGAGATGTGTGCAATCTGCGAGTG
AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCACTTGAAGCTCCGCACTCCAAAGAAAGCAACAGAT
CACGAAAAAAGAGATGCGGCCCGCCGAGCCTCGTCTGTGCTGTGCGCAATGTCTCTCTCGTGGG
TGGAAGCTCGGCCTTCTGTGCGACACCGCCCTGAAGGCGAGTTCAGAGGGACCGAGGAACATCCGCCCA
ACATCATCTGGTCTGCTCAGGACGACAGGATGTGGAGCTGGGTTCATGTCAGGTGATGAACAGACCGGGCGG
ATCATGGAGCAGGCGCGGCGCACTTCATCAACGCCCTCGTGACCACACCAATGCTGCTGCCCTCAGGCTCTC
CATCCTCACTGGCAGTAGCTGCCAACACCAACACTACACCAACATGAGAAGTGTCTCTCGCCCTCTCGGCG
AGGCACGACGAGAGCGCCACCTTTGGCGTGTACCTCAATAGCAGCTGGCTACCGGACAGCTTTCTTCGGGAAG
TATCTTAATGAATACACAGGCTCTACGTGCCACCGGCTGGAAAGAGTGGGTGGAGCTCTTAAACATCCCG
CTTTTATAACTACACGCTGTGTGCGAACGGGGTGAAGAGAGACCGGCTCCGACTACTCCAAGGATTACCTCA
CAGACCTCATCAACATGACAGGCTGAGCTTCTTCGCGAGCTCCAGAAAGATTACCCGACAGGCGGATTCCTC
ATGGTCTCATGCGCATGACGCGCCCGACGGCCGTGAGGATTACGCCCCACATATTACGCGCTCTTCCAAACGCT
ATCTCAGCAGCATACGCCGAGCTACAACCTACGCGCCCAACCCGGAGCAACACTGGATCATGCGCTACACGGGGC
CCATGAAGCCCATCCACATGGAATTTACCAACACTGCTCCAGCGGAAGCGCTTACAGACCTCATGTCGGTGGC
GACTCCATGGAGAGGATTTACAACACTGCTGGTTGAGACGGGCGAGCTGGACAACAGCTACATCGTATACAACCG
CGACCACGGTTACACATCGGCCAGTTTGGCCTGGTGAAGGGAATCCATGCCATATGATTTGACATCAGGG
TCCCTTCTACGTGAGGGGCCCAACCTGGAAGCGCGCTGTCTGAATCCCACTCGTCTCAACATTTGACCTG
GCCGCCACCATCTGGACATTTGACGCGCTGGACATACCTCGCGATATGGACGGGAATCCATCTCAAGCTGTG
GGACACGAGCGCGCGGTGAATCGGTTTCACTTGAAGAAAGATGAGGGTCTGGCGGAGCTCTCTTGTGTG
AGAGAGGCAAGCTGCTACACAAGAGAGACAATGACAAGGTGGACGCCAGGAGGAGAATTTCTGCCAAGTAC
CAGCGTGTGAAGGACCTGTGTGAGCGTGTGAGTACAGACGGCGTGTGAGCAGCTGGGACAGAAAGTGGCAGTG
TGTGGAGGACGCCACGGGGAAGCTGAAGCTGCATAAGTGCAAGGGCCCATCGCGCTGGCGCGGACGAGAGCCC
TCTCAACATCTGTGCCCAAGTACTACGGGCGAGGCGAGCGAGGCTGCACTGTGACAGCGGGGACTACAGCTC
AGCTGGCGGAGCGCGGAAAAAATCTTCAAGAAAGATACAAGGCCAGCTATGTCCGCGAGTGTCTCCATCCG
CTCAGTGGCCATCGAGGTGGACGGCAGGGTGTACCAGTGAAGCTGGGTGATGCCGCCAGCCCGCAACCTCA
CCAAGCGGCACTGGCCAGGGGCCCTGAGGACCAAGATGACAAGGATGGTGGGAGTCTAGTGGCACTGGAGGC
CTTCCGCACTACTCAGCCGCCAACCCTATAAAGTGACACATCGGTGTACATCTAGAGAAAGACACAGTCCA
GTGTGACTGACCTGACATGCGCCCTGCAAGGCTGGAAGAGCAACAGCTGACATCGACACAGAGATTGA
CCCTCGACAGAAACAAATTAAGAACCTGAGGGAAGTCCGAGGTCACTGAAGAAAGAGCGGCCACAGAAATGTGAC
TGTGCAAAATGACTGACACACCCAGCACAAGGCCCGCTCAAGCACAGAGGCTCCAGTGTGATCTTTTCAG
GAAGGGCTCGAAGAGAGGACCAAGGTGTGGCTGTGCGGGAGCAGAGGCCAGAGAAAGAACTCCGACGTGCG
TCAAGCGCTCGACAACACACGACCTGCGAGCTGCGAGGCTGCGAGGCTTCAACCCGAGCTGGAACATGGACCTG
CAGACGGCGCTTCTGGACACTGGGCGCTTCTGTGCTGACACGGCCCAACATACACAGTATGTGTGAT
GAGGACATCAATGAGACTCACAATTTCTCTGTGATTTGCACTGGCTTCTAGAGTACTTGTATCTCA
ACACAGCCCTACAGCTGATGATGAGTGAACACTGGACAGGAGTGTCTCAACCGACTACACAGTACAG
CTCATGGAGCTGAGGAGCTGCAAGGTTTACAAGCATTAACCCCGGACTGGAACATGGACCTGGATGGAG
AAGCTATGAGCAATACAGGCAGTTTCAAGCTCGAAAGTGGCCAGAAATGAAGAGAGCTTCTTCAAACTCACTGG
GACACTGTGGGAGGCTGGGAGGTTGAAGAACACAGAGGTGGAGCTCCAAAGAACATGAGGCGATCACTGA
CTGCACAGGCAATGAAGAACACTGTGGTGATTTCCAGCAGAGCTGTGCTATTTGGCCAGGAGGCTCGAGAAAGC
AAGCAGCAGCTCTCATCAACATGACAGATTCTGAGGATTAACAGCAGGAGGAGAGATACCTTCAGGAAGTCTC
ATTTTGGCCCTGCTTTCTTTGGATTATACCTCACCAGCTGCACAAATGCAATTTTGTATCAAAAGTCC
ACCACTAACCCTCCCCAGAGGCTCAAAAGGAAACAGGAGAGCGAGGAGAGAGATTTCTTGGAAATTTCT
TCCCAAGGGCGAAAGTCAATGGAATTTTAAATATCAAGGGGAAAGCAGTCTGTGTTCTTAATCTCTTAATCTT
TTGGTTTGTCAAAAGAGGAACTAAGAAGCAGGACAGGCAAGCTGGAGAGGCTGAAACAGCTGACGAGAGC
TTTGCAATGAGTCAAGTGCACAAAGAGATGACATTTACATGACATAAAGCTGTTGGCTCTGAAGAA
CTGCCTTCATTGTATATGTGACTATTTACATGTAATCAACATGGGAATTTTGGGGAACTTAATAAGAAAT
CCCAATTTTCAGGAGTGGTGTCTCAATAAACGCTCTGCGGAGCTGAAGAGAA

FIGURE 47

MGPPSLVLCCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIIVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPDKHIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPIEFDIRVPFYVRGPNVEAGCLNPHIVLNLIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVNRFHLKKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQVRKDLQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGQGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSAIEVDGRVYHVGLGDDAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDLDLYKS
LQAWKDHKLHIDHEIETLQNKIKNLREVRGHLKKRPEECDCHKISYHTQHKGRLKHGSSSL
HPFRKGLQEKDKVWLLREQRKKKLRKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
PFCATSANNNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

FIGURE 48

AACAAAGTTTCAGTGACTGAGAGGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
GCTGCTGGGCAGAGAGGGGACTGTCCGGCTCCAGATGCTGGGCCTCCTGGGGAGCACAGCCC
TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGCCACC
TGCCTTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
CCGAGTCCGCCGGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTCACC
ATCACCGTCATCCTGGCCACGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
CCCCGCCACACCCCTCACCACCTCCACCACCACCACCACCCCCACGCCACCATCCCCGCCA
CGCTCGCTGAAGGCTGCTGTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
TTCCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTTGCATGGCATGCCCCAGTGTAATATGGC
AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGTTTGGGGAGTGGAGAGCAAGG
GTGCTCTTTTCGGGGCTGGACAGCCCGTCTTGTGACAGTGACTCCAGTGAGCCCCAGAAATG
ACAAGCGTGCTCTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGTCTTGACCTCCTC
ATCAGGCTGCTGCAGGCCTTGCGGGGCAGGGCACTGGGAGAGGCCCTGAGAATGTCCTTTT
GGTTTGAGAAGGCAGTGTGAGGCTGCACAGTCAATTTCATCGGTGCCTTAGTCCAAGAAAAAT
AAAAACCACTAAGAAGCTTTAAAAAAAAAAAAAAAAAAAAA

[illegible][illegible]

FIGURE 50

GGCGGCTGCTGAGCTGCCTTGAGGTGCAGTGTTGGGGATCCAGAGCCATGTCGGACCTGCTA
CTACTGGGCTGATTGGGGGCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
GTACTCAGGGCTACTGGCTGGGGTGAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGGCTTTTCACTGAGAGC
TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
CCCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
CTGAGCTCATCGACCTCTACCAGAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
CATGTGGTGACAGCCACCTTCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
TGTCCTATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
AGATCTACCAGGAAGACCAGATCCATTTCATGTGCCCACTGGCAGCGGAGGAGACTTCTAT
GTGCCTGAGATGAAGGAGACAGAGTGGAAATGGCGGGGCTTGTGGAGGCCATTGACACCCA
GGTGGATGGCACAGGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGAAGTGAGCC
CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTACCTGGGGCGAGCAGCCGTGGCTGGGAT
GACGGTGACACCCGAGCGAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
GGAGCTGGACTTGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCCTGGGACTGAGC
CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAGTAACCC
ATGGCCTGCACCTCTCGAGTGCAAGTGGCTGCTGAGGAAGTGGAGAGCTCTCCAGCAGACTCT
CCAGCCCTCTTCTCCTTCTCTGAGGAGGAGGGGTTCTGAGGGACCTGACTTCCCTTGC
TCCAGCCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
GGGACTATTTCTGCACAGCCCCAGGGCTGCCGCCCTGTTGTGTCTTTTTTTCAGACTC
ACAGTGGAGCTTCCAGGACCCAGAATAAGCCAATGATTACTTGTTTCACCTGGAAAAAAA
AAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGLYGETGR
LFTESCSISPKLRSIAVYYDNPHMVPPDKRCVAGSILSEGEESPSPELIDLYQKFGKVFVS
FPAPSHVVTATFPYTTILSIWLATRRVHPALDITYIKERKLCAYPRLEIYQEDQIHFMCLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSPGSRETSAAATLSPGAS
SRGWDDGDTRSEHSYSES GASGSSFEELDLEGEGLGESRLDPGTEPLGTTKWLWEPTAPEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCCGAACAGCCTGTCTGTGGTCCCCGGCTCCCT
 GCCCCGCGCCAGT**CATG**ACCCTGCGCCCCCTCACTCTCCCGCTCCATCTGTCTGTCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGA
 GACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCTCTGGTTATAGAACTTGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTCCTCTGGTAG
 GGATGGCCATGGTGCAGCCCTCCTGGGCCTCATTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAAGAAGCTCAAGGAAGAGAAACGAACAAGAGCAAAAAGAA**TA**
ATAAATAATAAAATTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

MTLRPSLLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRAIIPSHLAYGKRGF
PPSPADAVVQYDVELIALIRANYWLKLVGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKKK

FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCTGGTGCCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCCTGCGCCCCCTACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGACC
CTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCCGCTGCTTTTGGAGA
CACGCTTCACATACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGGGCATTGTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCCTCTTGGGCTCATTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAAGAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTAAAAAATTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAATACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGCCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAAGCTAAAA

FIGURE 56

CTGCTGCATCCGGGTGCTCTGGAGGCTGTGGCCGCTTTTGTCTTTCTTGGCTAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGCCGACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAA**ATG**CTCTGGATTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCACCATGAAAGATTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCTCGAATTGCTGTATTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGCTGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAG**TGA**ACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGGTTTGTCTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTTGTGTAATACT
 AAAATCACGAGAACCTTAACACAACCAAAAAATCTATGTGGTATGCATTGATTAACCTT
 ATAAAAATGTAGAGGAACTTTCACATGAATAATTTTGTCAAATTTTATCATGGTATAATT
 TGAAAAATAAAAAGAAATTACAAAAGAAATATGGATTGTCAATGTAAGTATTGTGCATA
 TCTGAGGTCCAAACCAATGAAAGTGCTCTGAAGATTTAATGTGTTTATTCAAATGTGGT
 CTCCTCTGTGTCAAATGTTAAATGAAATATAACATTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATCTTCTCACTATAATTGGTATTTACTTTTACCAAAATCTGTGAACATGTAAT
 GTAAC TGCTTTTGGGGTCTCCCAAGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTTCCGCTGTGCCTCTCATT
 CCAAGGGCAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

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FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKEK
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

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TTCTTGGCTAAAATCGGGGAGTGAGGCGGGCCGGCGCGGCACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAATGTCTGGATTCTAGAGGGCTTGAGATG
CTCAGAAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCACCATGAAAGAT
TTCACCACCTCATACCATGCCTGTGGTGTATAGCAACCATAGCCTTCCATAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCAATTGGCTTTTCGTTGGTTTACATGTTGCCCTTTGGATCTCTGATTGCATCTATGTGG
ATTTCTTTTGGAGGTTATGTGTCTAAGAAAAAGACATAGTATACCTGGAATTGCTGTATT
TTCCAGAAATGCCTTCACTTTTTTGGAGGGCTGTTTTTAAGTTTGGC

FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTNTAGAGGGNTTGAGATGTTCAGAATGCATGAC
TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCAACCANTCATACC
ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTGGCTTTT
CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTGGAGGTT
ATGTTGCTAAAGAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCCTC
ATCTTTTTTGAGGGCTGGTTTTTAAGTTTGCCGCACTGAAGANTTATGGCAGTG

GGACACCGGGTTCGGACCAATGCANGACGGGTGGANTGACCTGAAAAAATGTTTGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGTGTACTATTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
CTTTGGGTCAAACAGGTGNTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
GATTGTGNATTCATGCGGATCTTCTTGGAGGTTATGTTGCTAAGAAAAAGACATAGTAT
ACCTGGAAATTCNTATTTTTCCGAAATGCC

FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTG
TTTGGGTCAAACAGGTGNTNGCATTTGGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

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FIGURE 62

GGGAGGCTGTGNCCGTTTTGTTTTNTTGGCTAAAATCGGGGGAGTGAGGCGGCCCGCGCGG
CGNGACACCGGGTTCCGGGAACCATTGCACGACGGGGTGGACTGACCTGAAAAAATGTTG
GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
TATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
GGTTGCTCTGGGCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
ATNTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

FIGURE 63

TGACGCGCGGCTG**GAT**CTGGGGCTTCGCGTGGTCTGCTCCTGGCTGTGCTGCTGCTGCGGCGTCC
TGTCCAAAGTTTACTTTGGGACTATCTTCGGACAGTCCCCGAACTCTTTCTCCGAAGATGTC
AAACGGCCGCCACAGCGCCCTGTGAATCTGACAGGAGGCGAGGAAGAGGTTCTCAAACAAAGC
TTTTTTCAGCAACCAACTGCTCGAGGAAGCTGCTGTGGTGGTAAATGGCAGTGGCTTTGGGG
CGCTGGCTCGAGTCGAATCTTAGTAAAGCTGGCAGCACTGCTGGTGTGGGAACAACTAC
ACCAAGGACGAGGGGCTGCTGTACATCTTTGGAGAACTCTTGAATTTGACACAGGAAT
CCATTTACATTTGGCGGTATGGAAGAGGGGACGATATGGCCGCTTTATCATTTGTAGAGATCACT
AAGGCGACCTGGAATGGGCTCCCTCTCTCTCTTTTGACATCAAGTGTGAGAGGGGCGC
AATGGCCGCAAGGAGTACCCCATGTACAGTGGAGAGAAGCGTCACTTTCGGGCTTGAAGG
GAAGTTTCCACAGGGAAGCATATCATTGACAATGATATAAAGCTGTGTAAGGTGTGTCG
GTGGAGGCCCTCATGCCATCTGTTCAAATTCCTCCCATGCCCTGGTTACGCTCTCGAC
AGGTTGGGGCTGCTGACTCGTTTCTCTCCATTCTCAAGCATCCACAGACGCTGGCTGA
GGTCTCGACAGCTGGGGGCTCTCTTGAGCTCAGGCAGTACTACCTACATCTCCCCA
CTTACGGTGTCACCCCAACCAACAGTGCCTTTTCCATGCACGCCCTGCTGTGTAACCACTAC
ATGAAGAAGGAGGCTTTTATCCCGAGGGGGTTCCAGTGAATTCGCTTCCACACCATCTCCGT
GATTACGGGGGCTGGGGGGCGTGTCTCAAAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAGAAGCTGTGGTGTTCAGTGTGAAGAAGGGGCATGAGCTGTGAACATCTATTTC
CCCATCGTGGTCTTCCAAGCGAGGACTGTTTCAACACCTATGAACACCTACTGCGGGGAAGCGC
CCGCTGCGCTGCCAGGCTGTGAAGCAGCAACTGGGGAGCGTGGCGCCGGCTTAGGACTGACCT
TGTTTTTATCTGCTCGGAGGACCAAGAAGACCTGCATCTGCGCTGCCAACTACTAT
GTTTACTATGACACGGGACATGGACAGGGGATGAGGCGCTAGCTGTCTCATCGCCGGGAAGA
GGCTCGGGAACACATCCCTCTTCTCTTCTCGCTTTCCCATGACGCAAGAATCGACCTGGG
AGGACCGATCCCGCGGGCTGACGCAATGATCTGCTCATACCCCTAGCCTACGAGTGGTTT
GAGGAGTGGCAGGCGGAGCTCAAGGAAAGCGGGGCGAGTGCATGAGACCTCAAAAAGT
TTTTTGTGAAGGCTCTATGTTCAGTGTGCTTGAATACGTTCCCAACAGCTGGAGGGGAAGTGTG
AGAGTGTGACTGTCAGGATCCCCACTCAACAACAGTTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGGCTGACCATGACTGGGGCGGCTGACCCTTGTGTGATGGCCCTCTTGGAGGC
CCAGAGCCCCATCCCAACCTCTATCTGCAGGCGAGGATATCTCACTGTGGACTGTGCG
GGGCGCTGCAAGGTGCCCTGCTGTCGACAGCGGCATCAAGAAGCGGAAGTGTGACTCAGAC
CTTAAAGATTTTGATTTAGATCTGGGCGACAGGCAAAAAGG**TAG**TTTCCATCAGGAGG
AGTCAAGGAAATTTGCCAATGGGCTGGGGCATCTCCCTTGACTTACCCATATGTCTTTTCTG
CATTAGTTGCTTTCGACGATATAAGACCTCAATTTGGTTGTGATGCTGAAGAGAGGCTAG
TTTAAATACCAATTCGGAATCTGGGGCAATGGAATCATGCTTCCAGCTGGGGGAGGTGAGA
TCTTTACGGCTTTTATAACATGCCATCCCTCATTAATAGGATATGACTTGAATGCTGATG
TCTCATGACGAGGCGGGCGCTGTCATCTGCGCTCAGGTCAGCTGCTCAACTCAGTGTACAAAGCGA
ATATTTCATCTGTGGATGAACCCCTGGGACATTTGTGAGCTCAACCTGGTGGGTTTCAGTTC
TGCTCTGAGGCTTCTGCTCTCATTTACTTTATGCTGACGCTGCACAGTGTCTACACTTCAAGG
GAAGGGGAGAGTAAATGAGGCTTAACTCAAACCTCTGGCGTGGTTTTGGTTGCCATTCCATA
GCTGCTCTCGCGCTGATCTGTTTGTGGCTGGGTTCAGTGGCTCTTCAGGGGACAGGAAAT
GGGTGCATCTCAGATGATCATATCACTGAGCTGGGGTAACAGCAGATCATCATGTAGTA
CTGGGGTCCAGACTGCTTCAATCTGGCACTGAGGACCTCGGGTCTGCTGCTCATGAC
CTTATCCCAACATCAACAGGGAAGGTTATGACGAGGAAGTGTACGCGAGTCTGACGCG
TGGACTGTGAAGTGAATACTTTGCTGGCTGAAGCAGGCTCAGGCGATTCGCGCGGCGG
CACAGAGGGGCAGTGCAGGAGGCTGTGGGTAAGGAGGAAGTACATCAGAAAAGGGA
AAGCCAGCGAATCTGTGTGAAGCCAGAAATGGCATTTGCAGTTAATTAGCACATGTGAGGG
TTAGACAGGTAGTGAATCAAGCTCAAGGTTTGGAAAAATGACTTTTCAGTTATGCTCTTTG
GTATCAGACATACGAAAGGCTCTTTTGTAGTGTGAGTGAATGACATTAATAAAATTTATG
ATTCCATTGCTTTAAAAAATAAAAAA

FIGURE 64

MWLPLVLLLAVALLLAVLCKVYLGLFSGSSPNPFSEDVVKRPPAPLVTDKEARKKVLKQAFSAN
QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNGLEFDTGIHYIG
RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
EEAII DKYIKLVKVVS SGAPHA ILLKFLPLPVVQLLDRCGLLTRFSPFLQASTQSLAEVLQQ
LGASSELQAVLSYIFPTYGVT PNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
GGAVLT KATVQSVLLDSAGKACGVS VKKGHEL VNIYCPIVVSNAGLFNTYEHLLPGNARCLP
GVKQQLGTVRPGLGMTSVFICLRGTKEDLHLPSTNYYVYYDTMDQAMERYVSMPREAAEH
IPLFFAFPSAKDPTWEDRFPGRSTMIMLIPTAYEWFEWQAE LKGRGSDYETFKNSFVEA
SMSVVLKLPQLEGKVESVTAGSPLTNQFYLAAPRGACYGADHDLGRLHPCVMASLRAQSPI
PNLYLTGQDI FT CGLVGALQGALLCSSAILKRNL YSDLKNLDSRIRAQKKKN

[illegible]

MRVRIGLTLLLCAVLLSLASASSDEEGSQDESLSKTTLTSDSVKDHTTAGRVVAGQIFLD
SESELESLIQEEDSLKSQEGESVTEDISFLESPNPENKDYEEPKKVRKPALTAIEGTAHG
EPCHFFFLFLDKYEDECTSDGREDGLWCATTYDYKADEKWGFCEEEAAKKRRQMGEAEMM
YQTGMKILNGSKKSQKREARYLQKASMNHTKALERVSYALLFGDYLPQNIQAAREMFEL
LTGEGSPKGTAGNFKLYASGLGVNSSQAKALVYTTFGALGGNLIAHMLVLVSRLL

FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCC**CATG**GCCTGCCGGTGCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTCTGGCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGCAGCCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCT**TAG**GGGTGGGGTGTGAGATGGGTGCCTCCCCCTCTGCCTCCATTCT
GCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNACVLTTISPVQPEDDADYYCSVGYGFSF

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
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CGCGCCCCGCCCCGAGTCCGGGCCCCGGGGGCGGGGCGGGCGGGATCGCGGCGCCGGGGCGCG
CGATGACCGCGGAGCGGACGACGCGCGGGGCCGGCCCTGACCCGCGCCCGCCCTGAGCCG
CCGCGCGAGGTCCGGACAGGCCGAGATGACGCGAGCGCCCTGCTGCTGCTCTGCTGCTGCGCG
CGCTGCTGCTCTGGGGGCTCTCCACACGGCCCGCCCGCCGCGCCAGAGCCGCCAAAGATGGCGGAC
AAGGTGTTCTCCACGGCAGGTGTGGCGCGCTGGGCGCGCATGTGCGGCTGCAGTGTCCCACTGAG
GGGGGACCCCGCCGCGCTACCATGTGTGGACCAAGGATGGCGCACCATCCACAGCGGCTGGA
CGCCCTTCCGCTGTGCGCGAGGGGCTGAAGGTGAAGCAGGTGTAGCGGGAGGATGCCGGG
GTGTACGTGTGCAAGGCCACCAACGGCTTCGGCAGCTTGAGGCTCAACTACACCTCTGCTGT
CTGGATGACATTAAGCCACGGAGAGAGAGAGCTGGGGGCCGACAGCTTCTCTGGGGGTCAA
AGGACCCGCCGACGACGACGTGGGACAGCCGCGCTTACACAGCGCTCCAAAGTAGGGCG
CGGGTGATCGACGCGCCGTGGGTAGCTCTGTCGGGCTCAAGTTCGCTGGCAGCGGGCACCC
CGCGCCGCACATCACTGCGGATGAAGACGACAGGGCTTGTACGCGCCGACAGGCGCGGTGAGC
CAGGAAAGAAAGATGACATCTAGCTCTGAAGAACTCGCGCGGGAGACAGCGGCACAAATAC
ACCTTCCGCGCGTGTGCAAGCCGCGGGCGGCATCAACGCCACCTCAAGGTGGATGTGATGCA
CGGACCGGTTCCAAGGCCGTGTCTCAGGACGCGCACCCCTGAAACAGCGGGTGAGTTCTCG
GGGGGACCGACGCTCTTCCAGTGAAGGTGCGACGACCTGAAGCGGGTGATCCAGTGGCTGT
AAGCGCTGGGATGACGCGCGGAGCGGCGCCACCACTTCCACATCGATGTGGGCGCGGAGAA
GTTTGTGTGTGCTGCCACGGGTGACGTGTGTTCTGCGCGGCCGACGGGCTCTCACTCAATAAGC
TGCTCATACCGTGTCCCGCAGGACGATGCGGGCATGTACATCTGCTTGGCGCCAAACACC
ATGGGTCACAGTCTCCGACGCGCTTCTCTACCGTGTCTGCCAGCAACAAAACCGCCAGGCGC
ACCTTGTGGCCTCTCTGCTTCCGCGCCACTAGCTTGCCTGGCCCGTGTCTATCGGATCCGAG
CCGCGCGCTCTCTTATCTTGGCACCCTGCTCTGTGGTCTTGCCAGGGCCAGGAAGAACGCG
TGCAACCCCGCGCTGCCCTCTCTCTGCTTGGGACGCGCGCGGGGAGCGCCGCGACGCG
CAGCGGAGACAGGACCTTCCCTGCTTGGCGCGCCCTAGCGCTGGCCCTGTGTGTGGGCTGT
GTAGGAGAGATGGTGTCTCCGCGAGCCCGCCAGCTTACTGGGCGAGGCCCGAGTGTGCTGCG
CTCAAGTTGTACCCAAATCTACACAGACATCCACACACACACACACACTCTCACAC
ACACTCACAGTGGAGGGCAAGGTTCACACAGCATCATCACTATGCTAGTGTAGAGCGGACCG
GTATGCACTGGGCGAGGGGGGGCGCGGAGACGAGGCAGCTGGGAGATGAGGACGGAGCT
GACAGCAAGGCGAGGGGACCATGCGGAGGAGGAATGCCAGACCCAGGCAGTGTGTGTG
TGAGGCGATAGCCCTGGACACACACACAGACAGACACACTCACTGGATGATGTATGACAC
ACACATCGCGCACAGCTGTCTCTTGAAGCCACAGTACGACAGCAGCATGCACAGATATG
CCGCTCTGGGACACAGATAAGCTGCCAAATGCACGACACAGCAGACAGAGATGCCGAAACA
TACAAAGACATGCTGCTGCATACATACACAGCACACCATGCGCAGATGTGCTGCTGGACA
CACACACACACAGGATATGCTGTGCGAGCAGACAGCTGCAGATATGGTATGCCGACACA
CAGGTGCACAGATATGCTGCTGGACACAGATAATGCTGCTTGACACACATGACACGG
ATATTGCTTGGACACACATACACACACGCGTGCAGAGATATGCTGTCTGGACAGCACAC
ACATGCAGATATGCTGCTGACACACACTTTCAGACACAGCTGCACAGGCGAGATATGCT
GCTGGGACACGCGAGATATGCTGTCTAGTACACACACAGCAGACATGCTGTCCGGACACA
ACACAGCATGCACAGATATGCTGTCCGACACACACAGCAGCAGATATGCTGCTGGAC
ACACACACAGATATGCTGCTTCAACTACACACACAGTGCAGATATTTGCTTGGACACACACA
TGTGCACAGATATGCTGTGGACATGCACACAGTGCAGATATGCTGTCCGATACACACG
CAGCAGACATGCAGATATGCTGCTGGGACACACTTCCGACACACATGCACACACAGGT
GCGATATGCTGCTGGACACACACAGATATGCTGCTCAACTCAACTCAACAGTGCAGTA
TGTGTGCTTGGACACACATATGTCAGAGATATGCTGTCTGGACATGCACACAGTGCAGATA
TGTTGTCCGATACACACAGCAGACACATGTCAGATATGCTGCTGGGACACACTTCGGA
CAGCATGACACACAGGTGCAGATATGCTGCTGGACACAGCAGACTGACGTGCTTTTGG
GAGGTTGTGCCGTGAAGCCTGCAGTACGTGTGCGGTGAGGCTCATAGTTGTAGGGAATTT
CCCTCGCTACCGCTCATCCCCAACTCTGCGCGCTGTGTCCCGCCCTCAGTCCCGCCCTG
CATCCCGGCTCTGTGCTCCTTGGCCTTATTTTGCAACTGCTTTGGTGGGCCAGG
AGTCCGCTACTGCTGTGGGCTGGGTTGGGGGACAGCAGCCCAAGCCTGAGAGGCTGGAG
CCATGGCTAGTGGCTCATCCCCAGTGCATTTCCCCTGACACAGAGAAGGGGCTTGTA
TTTATTTTAAAGAAATAAGATAATATTAATATGATGAAGGAAGAGCTGGTGTCAAGGAC
TGATGTTCTCTCTGGGCGCGGGACCGCGCTGTTCTTACGCACTGCTGATGACACACCCC
GTGACGGGACACACACCCCCACCCCACTGTGCTGTGGGCCGAGATCTCTGTAATTTTA
TGTAGAGTTTGAAGCTGAAGCCCGTATATTAATTAATTTATTTTGAACAAAAA

FIGURE 70

MTPSPLLLLLLPPLLLGAFPPAAAAARGPPKMADKVVPRQVARLGRTVRLQCPVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGSLSVNYTLVVLDISPGL
ESLGPDSSSGGQEDPASQQWARPRFTQPSKMRRRV IARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPEVL
TGTHPVNTTVDFGGTTSFQCKVRS DVKPV IQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLT VLPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTL LLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGS PAAPQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

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FIGURE 71

CCCAGCTGAGGAGCCCTGCTCAAGACACGGTCACTGGATCTGAGAAACTCCCAGGGGACCGCATTCAGAGTCT
 AGTGACTCTGTGAAGACACCACTACTACCTCTTGCCACGTTCCACAGGGCTTGGGGGAAAGATGCTGGGGACCA
 AGGCTGGGTGTCTCCTTCTGCTGAGTCTGAGTCTACATCTGTGTGGGGAGACAGACGATGCTCCGCACTCA
 GTAAGAGAGTCTCAGCTGGGAGAGACACCCAGCATCTTTGCCAGCTCTGCCAGCCCTCGAGAGCCCTGGC
 TGAGTGGACACATCTGACATCTGATCTACCCAGCGGGAGAGGGGACATGAGCGGTGGAGCCCATCTGCT
 TCTACTTATGGGACCGGTGTATGTGCCCTGCCCTCGGGCTAGAGGCTCGGACCTACTGGACACATCGGGG
 AGCACTGGCCAGGTGGTCTCATGGTAGTCCCGTGGGGGTCTTGTGTGCTCAACAGGAGAGAGCGGGCTGGCCA
 GAAGCTCTTAATTAACCGTACGCTTCCCTTGCCACACAGGATCCCTGGCCGAGACAGACAGCGCATCTGGA
 GCCATGGTCTGCTGGAGCAAGTGCTCAGCTGCTTGTGGTGCAGCTGGGGTCCAGAGCTCGCACAGCATTTGCT
 TTGGCAGAGATGGTGTGCGTGTGCTGAGTGGGCGCAGCGAAGAGGCTCAGCATGGGCGCAGCATGTGACAG
 CTGTGACTGTGACTGCCAATGGCGGAGTGAATGTGACTGTGTGGTCTGTGATGCCAGAGATCACTGCTTC
 ATGGGGCTGTCTCCTTCCCGGAGGTGCCCAGGCTCAGGGGCTGCTATCTACCTCTGACCAACAGCGCGAAG
 CTGCTACCCAGACAGACAGTATGGGAGATTCCGAATCCCTGGCTTGTGCCCTGTATGGCAAAAGCATCTGAA
 GATCACAAAGGTCAAGTTTGCCCCCATTTGTACTCACAATGCCAAAGCTAGCCTGAAGGACGCCACCATCAAGG
 CAGAGTTTGTGAGGCGAGAGATCTCATACATGGTGATGAACCTGAGACAAAAGCAGGAGAGCTGGGACAGG
 GTGTCTCTGTCTGTAGGCGCAGGAGAGCCCGCCAGCAAGATTTTGTGTATATAATGACACTTTGCT
 GGATCCTTCCCTCTACAGCACTGACAGCAGCTGT
 TTGTGAAGGCGCAGAGTGTGTGTGGGCTGTGAAGTCCAAGTTGCCAGCTGATTTGTCAAGACATCTGATGAG
 ACTCCTTGAACCCAGTTCTCGAGAGCTATCTTATCCGGCTGCCCATGATTGCTTTCAAGATGCCCACTCT
 CTCTACTATGACGTGGGAGCTGCCCTTCTTGAAGACTTGTGACGGGCGAGGAGATTAATGGATAGGCTGCCGTG
 ATGCTGTGACAGACTGCTGTGGCATCTCCAAGACAGAGAAAGGAGATCCAGTGCAGTGGCTACAGCTATCCC
 ACCAGGTGGCGAAGGAGTGCAGCTGCCCGCTTGTGAGAACCTGAGGACTCTGTGGCGGCGCTCTCAAGTGC
 TCTGCAATAGGGGAGCCATGCGCTTTGGCATGTGTACATGGGCAAGCGGCTGTAAAGCATCACTGGCTACA
 AGGGCACTTTCACCTCCATGTCCCCAGGACACTGAGAGGCTGGTGTCTACATTTGTGGACAGGCTGCAAGAG
 TTGTGCAACACCCAAAGTGTCTACCTTTCAACAAAGAGGGGAGTCCGCTGTTCCATGAATCAAGATGCTCTG
 TCGAAAGAGGCCATCACTTTGTGAAGCCATGGAGACCAACATCATCCCCCTGGGGGAAAGTGGTTGGTGAAGAC
 CCAATGGCTGAAGCTGGAGATTTCCATCCAGGAGTTCTCAGGCGAGATGGGGAGCCCTAGATAGGAAGTGAAG
 CGCAGTGCACCTCTGTGATCCCGGATAATTTCCACAGCGACAGCTGCCAGCATGACCTGCACTTCACTCAA
 TGACGAAGGAGACACTTTCCCCCTCGGACGTATGGCATGTCTCTGTGAGCTCAGAGATGAGGTCACTCTCA
 AGCCACTTAATGCTGCGCAAGTGAAGGTCCACCTTGACTCGACCAGGTCAAGATCGAGAGGCATATCCACA
 GTGAAACTCTGGTCACTCAATCCAGACACAGGGCTGTGGGAGGAGGAGGTGATTTCAAATTTGAAATCAAG
 GAGGAACAAAGAGAGACAGACAACTTCTGTGGTGGGCAAGCTGGAGATTCTGTGAGAGGAGGCTTTTAAGCTGG
 ATGTTCTCCGAAGCGCGGGTGTCTTGTAGCTGAGGGCTACCGGAGTGAGAGGTCTTCTGCTAGTGAAGCAG
 ATCCAGGGGTTGTGATCTCTGATTAACCTGGACCTCACTGCTCTCTCTCAACCTTAGGGCTGGG
 CGCCTTTGACAGTGTGATCAACAGGCGCCCAACGGGCGCTGTGTGCTGCTCTGTGATGACAGTCCCTGATG
 CCTACTCTGCTCTATGCTTGGCAAGGCTGGCTGGGGGAGAACTGCAAGCAGTGGAGTCTTCTCTAAATCAAC
 CCAATGCAATTTGGCGTCCCTCGACCTTATCTCAACAAAGCTCAACTACCGTCGGACGGACCATGAGGATCCAG
 GGTTAAGAAAGACAGCTTTCCAGATTAGCATGGCCAGCAGAGGCCCACTCAGCTGAGGAGAGCAATGGGGCCCA
 TCTATGCTCTGTGACAACTCTCGGATGTGAAGAGGACCACTGACCTGACGCCCATCTCGGCTCTACAGATT
 GAGGGGGATTCGATTAAGTACTACAAACAGTCCCTTCAACAGAGTCACTTACCTGAGCTGAGCAATATCT
 GGCATGGTGGCCAAAGCCGATGGAATTGAGGCTGCTATATCAAGGTGAAGATTGTGGGGCCAGCTGGAAGTGA
 ATGTGCGATCCCGCAACATGGGGGGCATCTATCGCGCGCAGTGGGGAAGCTGTATGGAAATCCGAGATGTGAG
 AGCACTCGGGACAGGGACAGCCCAATGTCTCAGCTGCCCTGTCTGGAGTTCAGTGCAGTGGGATGCTCTATGA
 TCAAGACCTGTGACCGCAGCACTGGTGAAGTCTATCCCGAGGCGACTGCGCTGAGCGAGCTGTGAACCCCA
 TGCATGATGATGACTGACCAACACTTCCAGCTGGACCTGACACAGCAGCAAGTGAAGTCACTGCTGTGCA
 CCGCTTGGACCACTGGGCGCAACATATGGCATCTACACTGTCACTGACCAAGGACCTCGCACCGCCAGGAGAT
 CGCGCTCGCGCGGTGGTTTGTATGGCACATCCGATGGCTCCTCAGAATCTGAGAGCAATGTGGGAGTAGGCC
 TCACCTTCAACTCTGTATGAGAGGCGAAGTAGGCCCGCAGAGTGCTTCCAGTACCTCCAAAGACCCCGACAGG
 TCCCTGTCTGAGGACGCTCCAAGGAAGTGGCCCTCAGAGGACGAGGAGGAGGAGGAGGCTGGCCAGCG
 CAGGGTGGAGTGTGTGCTCTGAGATGCTGTGATGAGTCTGTCAACAGCTGATACATCAATTTGTGCT
 ACTTCAACCTCTGCTTCTGCTCAATTCATGTGACAGCATTGTGACAGTGTGACCAACTCTCACTTGTGTAT
 TTAAGCACTCTGTTTGTGTGAAATTTGCTTGTGTTTCTTCACTGCCCTTACTTCTTGTGCTGCTACTGAT
 TTGGCACTGGCCCGCAACATGGCACAAATAAGGCCCTTTGTGAAACTGTCTTTAAATGAAACAGCAAAAT
 GGCCATCGTGAATAACTTGCAGCTTCAACTGTACTTCAATTAATGCCATTAATGCAATATACCTTCTCTCTT
 TTTCATGTTTGTGCCACCTTCTGCAATAGTGATTAATCTGATGCTGAAGATCAATTAACATATAAGGACAT
 TTCTTGGCTCTGCTGACAGACATAGGCAAGCTTGTGATGATGCTCTACATATAAGTGCCTGATTAAG
 AATAAACAACAATACTTTACTTGAATGTAAATAACTTATTATTTCTTGTGAATTTGAAATTTGAACTGAGT
 ACATTCAAGTTTAAGCTATTAAATATAGGGTGATCAATAGTTCTCTACCAAGTCTGGAAGAGCACTCTGGT
 ATCCACAATTACCAAGGTTGCTAACTGTATTTGTACATTTCCCTTGTACCTTGTGTTTGTGTTGTCAGAAAC
 CCAGTGTAGCCGAGGCGAGTGTCAATAAATGCATACTCTGTAATTTCCGAAAAA

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPEGWTTWFNI
 DYPGGKG DYERLDAIRFYYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSREGFWCLNREQ
 RPPGNCNSYTVRFLCPFGSLRRDTERIWSPPSWKSCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAIYLLTK
 TPKLLTQTDSGRFRIPGLCPDGKSIKIKTKVFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPKYFWYHNDTLLDPSLYKHESKLVLRLKQQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQNATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNCCKISKTEEREIQCSGYTLPTKVAKECSCQRCETETRSIVGRV
 SAADNGEPMRFHGVYMGNSRVSMITGYKGTFTLHVPQDTERLVLT FVDRLQKFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVVGEDPMAELEIPSRSFYRQNGEPIYIGKV
 KASVTFLDPNISTATAAQTDLNFINDEGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAYRSEFLPSEQIGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNNAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDINTVFPN
 EDDPMSWTEDYLAWWPKMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLVKVIPQGSRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQS PAAGTVQGRVPSRRQQRASRGGRQGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAAGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCTCAATATACCTGAATACGCAC
 AATATCTTAACCTCTCATATTTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTATAAAAAAATACAGAG
 ACCTACCTACCCGTACGCATACATATATGTATATATGTAAGTACGACAAAGATCGCAGATCAATAAGC
 AAGCTCGCTTTAGTTTCCAAGAAATACAAAGAATTTAGAGATGTTATTTGTCAGAGTCCCTGTGCGATTGATG
 CCCTTTGGGTTACGGTGTCTCAGTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTTATGATTGTGTAAAGT
 CAGATTACACGGGAAGGGAAGTTTGGGATTTACATGGCCTGCCAGCCGGAATCCAGCGCATGACAAATAA
 TCTGAAAGTGAAGTTCGATCTCCGGATATTACCTGTGGAGACCTCTGTAGACCTCTGTGCAATGGGCAATC
 CCTACATGTGCAATAATGAGTGTGATGCGAGTACCCTTGAGCTGGCACAACCCCTTGAGCTGATCTTTGATTTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCACTTGAAGGAGTATCCCAAGCCTCTCCAGGTTAACT
 CACTCTGTCTTGGAGCAAAACCATTTGAGCTAACACAGACATAGTTATTACCTTTGAATCTGGGCGTCCAGACC
 AAATGATCCTGGAGAGTCTCTCGATTATGGAGCAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATCGATCTTAATCCGTGAAGGATTTATCAGCAGCATACGCTCTTAGAATCATTTGACACAGA
 AGAGTACTCAACAGGGTATACACAAATAGCAAAATAATCCACTTTGAAATCAAAGACAGGTTGCGCTTTTGG
 CTGGACCTCGCCTACGCAATATGGCTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTACAGACCTTGAGGATAAGGCTGTTAAGACAGCCGCTTGGGAAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGTAACTCCATGCCACTGTATGGC
 TGTATGACAAAGCAAAATGACATGCGAATGTGAGCACAACACTACAGGTCCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTGGAGTCCAGGCTCCTATCTCCCATCCCCAAAGGACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTTGGTACGAATGTCTGCGACAACAGACTCCTGCACTGCCAGAACGGAGGGACGTGCCACA
 ACAACGTGCGCTGCTGTGCGCCGGCCGATACACGGGCATCCTCTCGAGAGAGCTCGCGTGCAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCCAGGGCGCGCCCGCACGGCACCCAGCGCTGCTGCTGTGACACGCTGCT
 GGGACCGCCAGCCCTCGTGTTC**Tag**GTGTCACTCCAGCACACCGGACGGGCTGTGCCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAACATAGGAACAACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTCAAGTGAACATAAGCCATATTTATCACCCTGGACAGCACATCGAGCTCAAGACTGTTAATTC
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACATTTGCCAGCTGCAGAGCATATTGGGA
 TTGAAAGGCTGCGACAGCCGCCAAACAGGAAAGCAAAAAACAAACAAATCAACCGACTTAAAAACATTTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACCAATAGCAATTCITTTGCTGTGAG
 GTGCTTTGTGGGCATAAGGAAATCTGTTACAAGCTGGCATATTGGCCTGCTTCGTCCTGAATCCCTTCCAC
 CTGTGCTTTAGTGAACGTTGCTCTGTAAACCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGACA
 TGTGTAAACAGCCCTCTAAAGGCGCAAGCCAGTCATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACCCCACTATACAAGAGTGGCTATAGGAAAAAAGAGTGTATCTATCCTTTTGTATTCAAATGAAGTT
 ATTTTCTTGAACACTGTAAATATGTAGATTTTGTGATTTATGGCAATTTGGTGTACAGACCAATCTGTTAAT
 GTATCTAATCGAATCAGCAAGACTGACATTTTATTTTGTCCTCTTTGCTTTCTGTTTGTGTTCACTGTGCA
 GATTTCTCTGTAAGGCAACGAGCTGCTGGCATCAAGAAATATGATTTTACATATATACAGAGTGTAAATAGA
 TTCCACAAAGGCAATTTCAAATGTTTCTGTTGCTTTAAACCTGGAAGATTTAAAGAAATAAAACCTCTCGA
 TAAACGATTTAGCAATTTGTATTTGCAATTTCTTAAGATGAAGGAACAGCCACCAAGCACTTTACACTCAT
 TTAAGTATTTCTGTGTGAGTGTGATCACTTACGCTGACGATTTAGTTCCAGGAAGATGATTTGATGTTCACT
 AGCTTGGACAACTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATACACAGCAAAAAA
 AAAAAA

MYLSRSLSIHALVWTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLYK
VKLDFPDITCGDPPEFTFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
EYKPLQVNIITLSWSKTELTNDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
HMDPKSVKDLQSHTVLEICTEESTGYTTSKIIHFEIKDRFALFAGPRLRNMAASYGQLD
TTKKLRDFFTVTDLRIRLLRPAVGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
SKLTCECEHNTTGPDCGCKKNYQGRPWSPGSYLP PKGTANTCIPS ISSIGTNVCDNELH
CQNGGTCNNVRCLCPAAYTGILCEKLRC EEAGSCGSDSGQAPPHGT PALLLLTTLTGAS
PLVGF

FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCTCATGACTT
 CTCTTGTGGACCATGTCCGTGATCTTTTTTGCCTGCGTGGTACGGGTAAAGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGCAGACTGGCCAGTATCCAGGTGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTTCTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTGGAGACCCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTACACACCGATGCACCTTGAGGCTGCTCCTAATTTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCAACATCATGTGTGCTGCCCTGAATCT
 CATTTCGAGGAGTTACCTTTGCAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACCTCGTGAGCCAGCCACCCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTCTGCTGCTGGGGAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCATGTCAGTGAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTTGCCCAAGCGCCTTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCTTACATTTATATGATTTCTGGGGTT
 GCTTCAGAAGTGTATTTTCATGAATCATTATGATTTGATCCCCAGGATTCTATTTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGGCAAAACCAT
 TTACTTTACATATTCGTTTTCAATACTTGCTGTTTACATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
 TAAACTTGATAAAAGTGTTGAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTTTATTAACAAAAAAAAAAAAAAAAA
 AAAAG

FIGURE 76

MSVIFACVVRVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLETLWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

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TGCTTCCTGGAGACCCGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTAGAAAAGTGAAGTGGCATT
 TTAACATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAAAAAATTCAGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCCTCGTAGCGAGCCTAGTGGCGGGTGTTCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTAAACAGAGGCGGGTGGT
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCGCTCGTCTCTCCCGGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGCACACTGTACATCCTCTGCCACATCTTCCTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGTGCTGCTCCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCCCTCGGAACACTACTACATCCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCCAACCTGTCCCTCA
 TCTTCTCATGCCCTTGTCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGCTCTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGGTGTGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGCATCTCCTTCTTGGGGTTCTG
 CTGCTCCTGGTGTGTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGTGGAAGACCTGGAGGAGCAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGCAGGATCTGTAATCCTACTTCTGCTGGCTGCCCTTAGACATGGAGCTG
 CTACACAGACAGGTCTGCTCTGCGACACAGAGGGTCTGCTGGAGAAGAGGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTTGCTATGCTGTGCTTGGTGTCTGACCG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGCTGCTCATCGATGAGGCTGCCATG
 CCCCAGGATGCGAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCCGTATTACAGTTGTACTCATCTTTTACCTAATGGTGCCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGCCTGCGGCCAGATGGCAGCAGACTGCCATGACGAGATAATT
 GGGAACTGTGTCTGCTCCTGGTCTAAGCTCAGCACTTCTGTCTTCTCTCGAACCCCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTTCTACA
 TTGTGTTCTCTACAACGCAGCCTTTGCGAGGCTCACCACACTCTGTCTGGTGAAGACCTTC
 ACTGCACTGTGCGGGCAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCCGT
 CTCGGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCA**TGA**CCTCCAGCTGGGGGTGGGA
 AGGAAAAAACTGGACACTGCCATCTGCTGCCATAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAACTCTGAGAGGGTGGGTGGCGAGAGGGGAGCAGGCCATCTGCATATT
 GCATAATCTGAGCCAGAGTTTGGGACCAGGACCTCCTGCTTTTCCATACTTAAGTGTGGCCT
 CAGTATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAATCTGTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCATAGCCATGTTTACATGATTGATGTGCAAT
 AGGGTGGGGTAGGGGAGGAAAGGACTGGGCGAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCCCTGTGCCCGACAGAGCCTAAGCACTGTGCTATCCTGGAGGGGCTTTGGACCACCTG
 AAAGACCAAGGGGATAGGAGGAGGAGGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVVK
IALELCTFTLAIAGAVLLLPFSIISNEVLLSLPRNYIQLWNGSLIHGLWNLVFLFPNLSL
IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDKNKANRESL
YDFWEYYLPYLYSCISFLGVLLLLVCTPLGLARMFVSTGKLLVKPRILLEDLEEQLYCSAFEE
AALTRICNPTSCWLPLDMELLHRQVLALQTQRVLEKRRKASAWQRNLGYPLAMLCLLVLT
GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLGSGFAGVIQVVLI FYLMVSSVVG FY
SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
IVFLYNAAFAGLTTLCVLKTFATAAVRAELIRAFGLDRLPLPVSGFPQASRKTQH

FIGURE 80

GGCTGCCGAGGGAAGGCCCTTGGGTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCCGAGTGTA
TTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG

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FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTGC
CTGCCCTTTAAGGGCGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGGGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCACTGGACAGTTTGAAGGACACCCAGGCCCAT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCCCTCACTTGCAA
GGGATTTTCGCTTCTACTCACACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAACCCAGACAATATCCTTGAGGTTCAAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCTCTCAGTAGCCCTGTGCACTTGGATTTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACCTCTGGGCTCAAGTGATCTGCTCACCTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTCTGTGTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCCTTAATAAAAGAACTGACTTCAAAAAAAAAAAAAAAAAAAAAA
AAA

MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGFPHAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCCGCGCCCCCGGTGT
 GAGGCGGCCCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGTCTGTATACCTCATCGGGGCGGTGATTGCCGGACGAGATTTCTATAAGATCTTG
 GGGTGCCTCGAAGTGCCTCTATAAAGGATATTA AAAAGGCCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGGTTCGTGTGATAGTGAGAAACGGAACAGTACGATACTTATGTTGAAGAA
 GGATTAAAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTCACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATTC AAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACTTTGGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAAC TAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCGAATCAAAGTTGTCAAGCACCAATATTTGAAAGGAGAGGAGATGATT
 GTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCA ACTTTGACAAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGTATCAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTGGACTTTGTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTGTTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTCGATTCGGAAGAAATGACC
 AGCAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTCTGCCCTGAGT
 TTC AAGAATTAAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTTAGCAATTTCAATTCAAAATGCCA ACTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTTTTA

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
 AQEKFDLGAAYEVLSDSEKRRQYDITYGEEGLKDGHQSSHGDI FSHFFGDFGEMFGGTTPRQQ
 DRNIPRGSIIIVDLEVTLEEYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGGRFQ
 MTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGMETPFIFEGEPHVDGEPGDLRFRKIVVKH
 PIFERRGDDLTYNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
 NNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

FIGURE 86

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGGACAGAGGAACCATGGTT
CCGCAGAACNTGAGCACNTTTTGCCTGTTGNTGNTATACTTCATCGGGGCGGTGATTGCCGG
ACGAGATTINTATAAGATTTTGGGGTGCCTNGAAGTGCCTTNTATAAAGGATATTA AAAAGG
CCTATAGGAACTAGCCCTGCAGNTTTATCCCGACCGGAACCTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTGGGTGCTGCTTATGAGGTTNTGTCAGATAGTGAGAAACGGAAACA
GTACGATAATTATGGTGAAGAAGGATTA AAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTCACACTTNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGCACGAGGCGGCGGGGAGCTCGCGGGATGCGCCCGGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCTGCAGGTGTCGTGGAGGAACCTAGCACCTGCCATCCTCTTCCCCAATTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTCTGGCTTCGTTTGCAGCC
 TTGGTGCTGGTTTGCAGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCAATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTCACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCCTCCGTTGGACCCCAAACTCCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTCA
 TCACCTGGTGCTGGTGACAAGGAATGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAGGCCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**TGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTGCATAG
 TAAAGCAGGAGATCCCGTCAGTTTATGCCTCTTTTGCAGTTGCAAACGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACCTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTTATTTAGCTCACCTAGTGTTTCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTTAAATTAGAATTTCTGGCCTCTCTCGATCGGTGAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTGCAGGTTTGGGTTTGAAGCTGAGGAACT
 ACAAAGTTGATGATTTCTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVTVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSESEL
 ELDDVVITNPHEAILENEWIEDASGLMSHCIAILKICHTLLEKLVAMTMGSGAKMKTSAS
 VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTALLSVSHLVLVTRNACHLTGGLDWI
 DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLOEOSAI

FIGURE 89

GCTTCATTCTCCCGACTCAGCTTCCCACCCTGGGCTTTCGAGGTGCTTTCGCCGCTGTCC
 CCACCACTGCAGCCATGATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
 TTTGGAGTGTTTTCTTGTCTTTTGGAAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
 TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAAATGGTTTAGAAAGAACATTAGAT
 TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTCTGGGTGGTGTATTGTAGTC
 CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
 GGGCTTCTTTCCTGTCGTTGTGGCTTTATTAGAAGAGTGCCAGTCCCTGGATCCCTCCTAAAT
 TTACCTGGAATTAGATCATTGTAGATAAAGTTGGAGAAAGCAACAATATGGTATTAACAACA
 AGTGAATTGAAGACTCATTAAAAATATTGTGTATTTATAAAGTCATTTGAAGAATATTCA
 GCACAAAATTAATTTACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
 CCTACAAAGTACCAGCAGCAAAATTAGCAAAGAAGCAGTGAAACAGGCTTCTACTCAAGTGA
 ACTAAGAAGAAGTCAGCAAGCAAACTGAGAGAGGTGAAATCCATGTTAATGATGCTTAAGAA
 ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
 CTGTGGTGCCTGTTTCTTTTCTTTTTATTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
 TTTTAGAAGTGCCACTGCAATGGCAAAAATATTCCAGTTGCACTGTATCTCTGGAAGTGA
 TGCATGAATTCGATTGGATTGTGTCATTTTAAAGTATTTAAACCAAGGAAACCCCAATTTG
 ATGTATGGATTACTTTTTTTTGNCGNCAGGGCC

FIGURE 90

MISLTDTKIGMGLTGFGVFFLFFGMILFFDKALLAIGNVLFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPLGSLNLNLPGI
RSEVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTTCCCGGCTTCATTTCTCCGACTCAGCTTCCC
ACCNTGGGCTTTCCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTGAGATTCTTCTTCCAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTTC

FIGURE 92

GGCACGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
GGCTGCCAGGAAGGAGACGCCTTCTCTGAGTCTGGATCTTTCTTCTCTGGAAATCTTTGA
CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATC**ATG**GACCTCGCGGGACTGC
TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCCTTTATGCTCAGGGCTAATC
ATCAACACCATTAGCTCTTCACTCTCTCTCTGGCCATTAAACAAGCAGCTCTTCCGAA
GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
CGGGCACGGAATGCACCATCTTACGGACCCGCGCGCTACCTCAAGTATGGGAAGGAAAAT
GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCTGTCCGA
ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTGGCCAAGAAAGAGCTGGCCTATGTCCCAA
TTATCGGCTGGATGTGGTACTTACCAGAGATGGTCTTCTGTTGCGCAAGTGGGAGCAGGAT
CGCAAGACGGTTGCCACCAAGTTTGACGACCTCCGGGACTACCCCGAGAAGTATTTTTTCTCT
GATTCAGTGTGAGGGCACACGGTTCACGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTAGAAA
TAATGAAATCCAACACTGCTGGGAGTCTTAAACGGAAGAAATACCATGCAGATTTGTATG
TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGCTCGGCCTGGCTGCAC
AAGCTCTACCAGGAGAAGGATGCCTTTCAGGAGGAGTACTACAGGACGGGCACCTTCCAGAG
GACGCCCATGGTGCCCCCGGGCGCCCTGGACCTCGTGAACTGGCTGTTTTGGGCCTCGC
TGGTGCTCTACCCTTTCTTCCAGTTCCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
CTGGCCAGCTTCATCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
GACGGAAATTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGGAGGTGTCACCATCCGAAGGGAACCTTGGGGAACCTGGTGGCCTCTGCATATCCT
CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCTGCTGGGCACGGCGGAAGTCACGA
CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGAGGAAGATGTTTGTGAATCTTT
TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTCTTTTTGTGCGAGTGTGTGTGAGAATGGC
TGTGTGGTGAGTGTGAACTTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGTGAGTCTTCTGT
AACCCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATTATGCCTC
CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAAAAAA

FIGURE 93

MDLAGLLKSQFLCHLVFCYVFIASGLIINTIQLFTLLLWPINKQLFRKINCRLSYCISSQLV
MLLEWWSGTECTIFTDPRAYLKYKENAIVVLNHHKFEIDFLCGWSLSERFGLLGSKVLAKK
ELAYVPIIGWMWYFTEMVFCSRKWEQDRKTVATSLQHLDYPEKYFFLIHCEGTRFTEKKHE
ISMQVARAKGLPRLKHLLPRTKGFAITVRSLRNVVSAYVDCTLNFRNNENPTLLGVLNGKK
YHADLYVRRIPLEDIPEDDDECSAWLHKLYQEKDAFQEEYYRTGTFPETPMVPPRRPWTLVN
WLFWASLVLYPFFQFLVSMIRSGSSLTLASFILVFFVASVGVRRMIGVTEIDKGSAYGNSDS
KQKLN

100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0
100
90
80
70
60
50
40
30
20
10
0

FIGURE 94

CTGAGGCGGCGGTAGCATGGAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATCCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCCAGAAATATATTCCATGCTATCAGCTTTTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAAATCCGTCGTCATTGAGATCAGATCATGACGTTTAGAGAGAGGCTGCTTCACAA
 AAACCTGCAGGAGCATTTTTCAAACCAAGACCTTGTTTTCTGCTATTAAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGGTACCTTTAGTGGTTGCCAATCTGGGCATGCTGAACAACTGGGTATATAAAC
 TGATACAGGTTCCCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAAATGTATGCTTCATTA
 CAAGAGGAATTAAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAAACAGATTAAAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTCAGG
 CAGCAAGAGAGAAGAATCCAAAAAGACCTCAGGAGAACATTTTTCTTTGTCAGGCATTA
 CGGACCTTTTTTCCAATTCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAAATAGACA
 TGTTTCTAAAAGTAGCTGTAACCTACAACCACCATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCAAAATCATTAAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATTGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCCTACA
 TTTTGAFCCTTTTAAACCTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCAATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCCAACCTTTTTTTCACCTTTCTACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGAAAAGTGAGACCAGGCACAGTGGCTCACACCTGTAA
 TCCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGTCTATTAAAAAATAAAATGGAAAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAAATTTATATGAAAATTTATCTGAGTCATTAATTTCTCCTTAAG
 TGATACTTTTTTGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

FIGURE 95

MEGESTSAVLSGFVLJALAFQHLNTDSDTEGFLLGVEVKGAEAKNSITDSQMDDDEVVYITIDIQ
KYIPCYQLFSFYNSSGGEVNEQALKKILSNVKKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTPSIITESCSTRLEHSLYKPKGLFHRVPLVVANLGMSEQLGKYTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQDKPQENIFLCQALRFTFFPNEFLHSCVMSLKNRHVSKSS
KNYNHHLDVDNLTLMEVHTDIPEASFASTQIJKHALDLDDRWFQKRSRLDQTQDKRSA
NTGSSNQDKASKMSSPTDEIEKMGFGYESRSPTF

[illegible]

FIGURE 96

CGACAGACGCGCGGGCGGGGCGGAGCATGACGCGAGCGAGTGCACGCGGACGAGCGGACCGAGCGGGGACAC
CCAGACAGCGCGGACGAGAAAGCGCGCGCGGCCACACCTCTCGTGGTCCCGCGGCGAGCTGCCACCTTCCTC
CTCTCCCGCGGCTCGCGGCCCTCGCGGCCAGTGTCTGCGGCGTTCGCTGCCCGGAAACCCGAGGTCAACCA
GCCCGCGCCTCTCTCCCTGGGGCGCGCGCGCCTCAAGCGCCTCTTCTCCCTTGGCCCGGGCGCTGCGACCC
GGGGAGCGGCTTGCTTGACGCGAGGCGCCAGCTTACTTTGCGCCCGGCTCTCTCGCTCGCTGCTGCTCTCCAC
CAACTCCAACTCCTTCTCCCTCAGCTCTCGAGCTGCTAGTGTCCCGACTCCGCGAGCCTCGGCGCGGCTCGCGTA
CGCGCTCTCCGTCGGTCCGCTCCAAAGGTTGGAGCGGTCGCGCCGCCGCCGACCAATGCGACAGGTTGGCTTGC
CGCGCTTCTCTGCACCTGCGATGCTCGACGCGCGCTGTGCTGCTCGGAGTCAAGTTCGAAAGTTGCTCGG
AAGTGCAGCGCTTTTACGTGTCCAAAGCTTTCAACAAGAACATGCCCCCTCCAGAGTCAACGCTGATCAT
TTGAAGTCTGTGCCCGAGGCTTCACTGCTGCTCTCAAGATGAGGAGAGATACAGCTTACAGCTTAAAGACA
TGATTTCAAAGTGTGGTCAGGACAGCTGCATCACTTTGAAGCTGTCTTGTTCAAGCTTCAAGAAAGTGTG
ATGAATTTCTCAAAGACTACTTTGAAATCGAGAGAAATCTCGTAATGATATGTTTGTGAGACATATGGCCAT
TTATACCTCAAAATTTCTGAGTATTTAAAGACTCTCTTGCTAGCTTGAAAGCTTACTAGCTGTGTGGGAATGT
GAACCTGGAAAGAAATGCTAAATGACTTCTGGGCTCGCCTCTTGAGCGGATGTGTCCGCTGGTGAATCCGAGT
AACCTTTACAGTATGATATCTGGAATGTGTGACAGATGATACGGAGAGCTGAAGCCCTCTCGGAAGTGTCCCT
CGAAATGAAGTCCAGGTTACTCGTGTCTTTGTAGACAGCCGCTACTTTCTGCTCAAGGCTTACGGTGTGCGGG
AGATGCTGTGAGCAAGTCTTCGTTGGTAAACCCACAGCCCATGTACCATGCCCTGTGAAGATGATCATCT
GCTCCACTGCGCGGGTCTGCTGACTGTGAAGCATGTTAACAATCACTGCTCAAACATCATGAGAGAGCTTTTG
GCCAACCAAGGGCATCTGATATTTGAATGAAACAATTTCACTAGTCACTGCTGCTGATGTGGCAGAGAGCTGACA
GGTCTCTTTCAACATGTAATCGGTCTGGATCTGGATCACTCGATGTGAAGATTTCTGATGCTATGAGACATCAGG
ATCAATAGTGTTCAGGTCTCAGAAAGTTTCCAGGATGTGGACGCCGCCACCCCTCCAGCTCGAGCAATTT
TCTCGTTCCATCTCTGAAAGTGCCTTCAGTGCTCGCTCGAGACACATCACCCCGAGGAGAGCCCAACACACAG
AGCTGCGCATCTGTTTGACCGCATGTTTACTGATGTCAAGGAGAAATGAACACGGCCAGAAATATTTCTGCTCT
CCCTTCGAGGACAGTTTTCACAGTATGAGAGATGGCTCGAGGAAACGGCATAAGGATGACTGTGGAAGTGC
AAAGGCGAAAGCAGGTACTCTTTGTCAGTGCAGGAAATGGAATAGCCACACCGGCAACACCCAGAGTCCA
GGTTGACACGAGAGATACAGACATGATCTCTTGTAATCACTGCTCTCGAGTATGATGACGACAGATGACA
AGAAATGACATCAAAATGGGAACGACCTGGAATTTTGATATCAGTGTGAAGATGATGGAGAGGAAGTGAAGT
GCGCTGTGAGTATCAGCAGTGCCTCTCAGAGTTTGACTACAAATGCACATGACCTAGCTGGGAAGAGTGCCATGA
GAAAGCCGACAGTCTGTGTTGCGCTCTCGGGGACAGCGCTACTCTCACTGCTCTCTGCAATCTTGTCTCGG
TTATGACGAGAGATGGGAGATTAATCTCAAACTCTGAGAAAGAGTTGTTCACTCAAAAAGTTAAAGGACAGAGTT
ATCACTTTTCTACATCTGATGACTTGTGTTTTAAATGAATGGCAACAATGTACAGTTTTTTACTATGTGGC
CAGCTGTTTGAAGAGCTGACTGTTGTTTTCTTCATCAAGTTTGGGAGGAAAGGCACTGTGATTGAGTTGGT
TCTCTGCTCCCCAAACGATGTAAACGCTGGTTCACAGTGTAGGTACAGACATATGATTGTTGCTATTTGTGA
TTTTTATCACTCACTTTTGTGTTGTATGTTTTTCTCATTTGTTTGGTGGTTTTTTTTTCCAACTGTGATCT
CGCCTTGTTCTTCAAGACAAACAGGCTCCCTCTGGCAGCTAAATGTACGTTATTTCTGAAATATTAATA
CTGTGACAGAGCAAGTTTATTTATCATGTATCTTTATTAAGAAGAAAGGCCAAAAAGG

1. $\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

FIGURE 97

MARFGLPALLCTLAVLSAALLAAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSSELFKDLFVELKRYVVGNVNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPFQDVPKRLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLD FEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFGCGPPKPLPAGRISRSESASFARSARFRPHHPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLPSNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

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FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGGTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCTGAGAGCCCCGAGAAGAAAATTGATGACAGTGTCTGGGCTGCCAAGAAGC
AGTGCCCTGTGATCATTTCAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTGTAGGAGCTCTGAGCGCCCACTCTTCCAATTAAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTCTCCCACTCACTCTCCCACTGTACCCACC
CCTAAATCATTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTTTGTGCTCTC
TCTAGTGTCTTCTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAACTGTAGCTTCTAGCTAGTGTCAATTTAACCTTAAATGC
AATCAGGAAAGTAGCAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 100

A**AT**GGCTGTCTTAGTACTTCGCCTGACAGTTGTCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAATTCCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTATGGAATTTGATGATAATGAAGGAA
AACATTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTAGAAAAGTTAGAATAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA

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FIGURE 101

MAVLVLRLTVVLGLLVLFLTCTYADDKPKDPDDSGKDPKPDFPKFLSLLGTEIIEHAVE
FILRSMRSTGFMEFDDNEGKHSSK

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FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCCATGGACATCCTGGTCCCACCTCCTGCAGCTGCTGGTGTGCTTCTTAC
 CCTGCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCTTCAGCCAGATAAAAGGGCTTACAGGAGCCTCCGGGAAAGTGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCACCTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTGTGCTCTGTGCAGAGCCCAAGGAAGGTCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCACAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACCAGCCTATCTATCTTCCACTGAGAGGGACCTAGCAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGTGTGATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCTCTGAGGCTACACCCATGCGT
 CTCTAGGAAGTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGGACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

FIGURE 103

MDILVPLLQLLVLLLTLPFLHLMALLGCWQPLCKSYFFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALLELGCGTGANFQFYPPGCRVTCCLDPNPHFEKFLTKSMAENRHLQYERFVV
APGEDMRQLADGSMDVVVCTLVLCVQSPRKVLQEVRRVLRPGGVLFFWEHVAEPYGSWAFM
WQQVFEPTWKHIGDGCCLTRETWKDLENAQFSEIQMERQPPPLKWLVPVPHIMGKAVKQSFP
SSKALICSFPSLQLEQATHQPIYLPLRGT

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FIGURE 104

GTGGGATTATTGAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCTTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTGAGGAATTGTAGGGCCCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCCGTGTTGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGCCATTGCAGCTATAAACAGCATTGACACAACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTGACCTTAACTTTTGAAGGAA
 AAGTAAAGGAGGATCCTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGTTCTAC
 TTGCCAATTCTGGTTCCCGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCCTCTACTAAAGTTGTCATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAAGGAAAGAATTGTAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCCTGGAGTTTTTGTGCAAACCTGACGGAATGGAAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGACTGTATAGCAGAACCTTGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCCAGTGCTGGAACAGATATTACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCAACAGGCAAAATCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTCAACAGAAATTTGAAGTGAAGCAAGCATTTCTCAG
 GAAGTCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCGACAGAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGTTCCTT
 ACTACAAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTGCTAGCTGGTACAGA
 TAATTCAAACTGCTGTTGGTTTTAATTTTGTAACTGTGGCTGATCTGTAATAAACTT
 ACATTTTTT

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHNNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIIQHNTSRNVIFYIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVVEDPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLAGSITTPPLLIVFYQQHSTIDPMWNVRHLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK

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FIGURE 106

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GGGAGACAAGAGGAGATTCCGTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCTAAACTTTTGGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCTGGTTCCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTTCAGCCTCTAC
TAAAGTTGTCTATCCGTGGAGCAGGAAA

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FIGURE 107

CGACGCTCTAGCGGTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCTGCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCCGGGCGCGGGCTGCA
 TCCGCATCTCTCCATCGCTGCGTAGAGGGCGGGCGGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTTACTGGTTTTGCAC
 CATAACTTCCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTACGGAATTGTAG
 GGCTCAACCTATAGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTCAGCACAACTCGCTCCAATGTGATTTTCTACATTGTTACTCTCAACAATACA
 GCAGACCATCTCCGTCCTGGGCTCAACAGTGATTCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCTAAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTCTACTTGCCAATTCTGGGTTCCACGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTGAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAAACCAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACGACAGAATATAACTAACCACTGAAAAATGGATGAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTCCAGT
 GCTGAAAAACGATATTCACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAAAAATGGTATATCCA
 GACCCAACAGGCAAATTCACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAATTTGAACTGTAAGCAAGCATTCTCAGGAAGTCTGGAAGATAGCATCGCTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGAAAAAGATGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCTCCATCTGCCTTACCAAGTGTCTTCTACTACAAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAAAGTCTGTTGGTTTTAATTTT
 GTAACTGTGGCCTGATCTGTAATAAACTTACATTTTCAATAGTTAAAAAAGAAAAA
 AAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGGCCATACCAGAGTCCTGCGCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGCTGCGCTGTCATGGGGGCAGCCATCTCCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCCTGTCCTGAGAAGGCCCCACCACCCAGAGCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGCTTATGAGTTGGTGCTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAAGCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCCCTCCCCTGGTCCTCCAGTGTTTGCTGGATAATAAATGGAACCTATGGCTCTAA
AAAAAAAAAAAAAAAA

FIGURE 110

GTTTGAATTCCTTCAACTATATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCCTCCAAGCAAGTCATTTCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCCTATTTCATCTGTTTTGATAAATGATGTTGACACCTCCACCGAATTCAGTGGA
 TC**ATG**TCGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCTTTGGCC
 ATGATGTTTACCTTCAGATTTCATCACCACTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGTTTGTATCGTA
 TCCACAGGCATCAGGCAGTGTCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAAATCACAAATAAGCCATCAGCAGTGTCTCCTTCTCTGCTGTTC
 AGCCACTGTGGACATTGTCATCCTCATTTTCTTCTGGGTCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAACATGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGGAATATAAGCCCT
 TTCGGGCATTTCGGTACATGTGGTCGTACCATTTAATTGGCCTCATCTGGACTAGTGAATTCA
 TCCTTGGTGGCAGCAAATGACTATAGCTGGGGCAGTGGTTACTTGTATTTCACAGAAGT
 AAAAATGATCCTCCTGATCATCCCATCTTTCGTCTCTCTCCATTCTCTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTAAATCTCTGTGGTGAGGATCCGAGAATCATTGTCA
 TGTACATGCAAAACGCACTGAAAGAAGCAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGTGTTTCTGGTGTCTTGACAAATACCTGTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAATCT
 TGTCAGAAGAACTCAAGTCACCTTACATCTATTAAGTGTCTTGAGAGACTTCATAATTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGGCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACCTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAGGAGCAACAAATTAACAATGCAAGGGCACAGCAGGACAAGCACTCATTAAAGGA
 ATGAGGAGGGAACAGAACTCCAGGCCATTGTGAGAT**TAG**ATACCCATTTAGGTATCTGTACCT
 GGAAAACATTTCTTCTAAGAGCCATTTACAGAATAGAGATGAGACCACTAGAGAAAAGTT
 AGTGAAATTTTTTTTTAAAGACCTAATAAACCTATTCTTCCTCAAAA

FIGURE 111

MSGRTIILGLCILALALSLAMMFTFRFITTLVHIFISLVILGLLFVCGVLWWLYDYTNDL
SIELDTERENMKCVLGFAIVSTGITAVLLVLIFVLRKRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFVVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

[illegible]

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTGVHSNKETAKKIKRPKFTVPQINC DVKAGKIIDPEFIVKC
PAGCQDPKYHVYGT DVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYSNGVQSL
SLPRWRESFIVLESKPKKGVTYPSALTYSSSKSPAAQAGETTKAYQRPPIPGT TAQPVTLMO
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDL SFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPAT HFNLKTH TNSRDLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFTITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLQPLVKRVCDTDR LACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISD TDTRIGAVQYTYEQRLEFGFDKYSSKPD I
LNAIKRVGYWSGGTSTGAAINFAL EQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAAWAAQEELEVIATHPARDHSFFVDEFNLHQYVPRI IQNICTEFNSQPRN

FIGURE 114

CAGGATGAAC TGGTTCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCCTTTCCGGTGCCTCATCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCGCGCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATTGATGTGAACGCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTCC
 TCCAGCCTTTCCAGACCCCACTGGCATGCCATATGGAACAGTGAACCTACTTATCATGGCGTG
 AACCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCCTGAGCAGCCTCACTGGTGACCGGTGTTCAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGACGAGCATCGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAAC TACACCCGCTTCGATGACTGGTACCTGTGGGTTTCAAGTATGCAAGGGGACT
 GTGTCCATGCCAGTCTTCAGTCTTGGAGGCTACTGGCCTGGTCTTCAGAGCCTCATTGG
 AGACATTGACCAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGG
 GGCTCCCGGAATTCTACAACATTCTCAGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTCCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCCTGCCACGGGGGATCCCAACCCT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAATCAGCAAGGTGGAGTGCAGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTCTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACATGG
 GTCCACTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGCTGGGGGTAC
 TCTTCAACACAGAAGCTCACCCCATCGACCTTCCCGCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGGAGCAGGTC
 GAAATTTTCAGAAAAACACTGTTAGTTCCGGGCGCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAGGCAAGGGAGAGGAAGCCTGCCAAACAGAGGTCCCA
 CTCTCAGCTGCCCCAGTCAGCCCTTCACTCCAAAGTTGGCATTACTGGGACAGGTTTTCTCT
 AGACTCCTCATTAACCACTGGATAAATTTTTTATTTTTATTTTTTGGAGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

MPFRLLIPLGLLCALLPQHGHGAPGPDGSAHPAHYSFSLTLIDALDITLLIIGNVSEFQVRVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARK
LPAFQTPTGMPYGTVNLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSPMPVQSLEAYWPGQLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNI PQGYTVEKREGYPLRPELIESAMYLYRATGDPITLLELRDAVESIEKISKVECG
FATIKDLDRHKLDRMESFFLAETVKYLYLLFDPNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVDLMREFYSLKRSRSKFQKNTVSSGPWEPPARPET
LFSPEHNDQAREKPAKQKVPLLSCPSQPFTSKLALLGOVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAAGTCTGAGTCTACCA
AATGCAGACTTTTACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTGTATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCTTTGTGGCTTCATGCTGATCCTTGT
 GGTGCTGCCACTGTTGCTCTGGAATAAGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGG
 TGGTCTCCAGACACCTTGAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCCTGGAT
 CTCATAGGTTTGCGGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGATGTGACCTCTAGACTGGGGCTGCCACTTGCTGGCTGAGCAACC
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGAAGGCTAGAGGGAACTGGTGACACTCTACAGTCTGACTGATTACAG
 TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCACTTTCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACCTCAAGCCCAATGCCGTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGTGCACGCCACACTGAAAATGGGATGTGCATGAACCGGAGGATC
 CATGAACACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGGTAAAGTACAGAATTGAGCAATAAAAGGGCCACCTTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQFTTMVLEEIIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
TVYYSVEYQGEYESLYTSHIWIPISSWCSLTEGPECDVTDITATVPYNLRVRATLGSQTS
SILKHFPNRRNSTILTRPGMEITKDGPHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECEVEVQGEAIPVLVLAFAFVGFMILIV
VVPLEFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG
TCAAAGTGAAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
CTGCCCCCTCAGAACCCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCT
GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTTGAGTGTG
ATGTCATGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTGAGGCCACATTGGGC
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGAACCCTTTCGCGCGCAAGGG
GTTNGCGAACCCTTTCGCGCCGCTGGGGTATCTCTCGAGAAAAAGAGGCCCAATATGACCCAC
ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCGGCCACCTCCGGAACAAGCCATGGTGGCGGCGAGCGGTGGCAGCGCGCTG
 GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGGCGG
 TCAACATCCGGGGCAAACCTGGTGTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
 AATGTGGCCAGCGAGTGTGGCTTACAGAGCCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
 AGACCTGGGGCCCCACCACTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
 AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTCCCC
 ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
 GACTTCTGGGAAGGAGCCCCACCTGGAACCTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
 TGGTAGGGGCTTGGGACCCAACTGTGTCAAGTGGAGGAGTCAAGACCCAGATCACAGCGCTC
 GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTTATATAACCACCGCGTCTCCTCCTCCACCA
 CCTCATCCCGCCACCTGTGTGGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
 AGACCCACTGACTCTCCTTTCCTTTACTCTTATGCCATTGGTCCCATATTCTTGTGGGGGAA
 AAATTTAGTATTTTGTATTATTTGAATCTTACAGCAACAAATAGGAACTCCTGGCCAATGAG
 AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
 TAGAAGTATATCAAGCAATAATCTCCACCCCAAGGCTTCTGTAAACTGGGACCAATGATTAC
 CTCATAGGGCTGTTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
 CAAATAGGAGGCATTCAATGAACATTTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
 AAAAAGTGCATCCAAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
 GTTATTTCTCTGTATTATTTCTTCATTACAAAGAAATGCAAGTTCATTGTAACAATCCA
 AACAATACCTCACGATATAAAAAATAAAATGAAAGTATCCTCCTCAAAA

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FIGURE 120

MVAATVAAAWLLLWAAACAQQEQDFYDFKAVNIRGKLVSLSEKYRGSVSLVVNVASECGFTDQ
HYRALQQQLQRDLGPHHFNVLAFCNQFGQQEPDSNKEIESFARTYSVSFPMFSKIAVTGTG
AHPAFKYLAQTSKKEPTWNFWKYLVA PDGKVVGAWDPTVSVEEVRPQITALVRKLILLKREDL

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FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAAGGCAAGCGAGCCATGGCTGTCTACGTCCGGATGC
 TGC GCCTGGGAGGCTGTGCGCCGGGAGCTCGGGGTGCTGGGGGCCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCTCAGTTCAGAGAGGTTGGATCG
 CATGGTCTCCACGCCCATCGAGGCCTCAGCTACGTTCAAGGGTGCACCAAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCCTGGAGACCAAGCACAGAGGGTCCAGAACGAGAGGCC
 TTGGTCTCTCCATGAAGACGTGAGTTGACCTTTGCCCAACTCAAGGAGGAGGTTGGACAA
 AGCTGCTTCTGGCTCTCTGAGCATTTGGCTCTGCAAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAACCTCCTATGCATGGGTGCTCATGCAAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACAGGCTATGGAACCTGGAGTATGTCTCAAGAAGTGGGTGCAA
 GGCCCTTGTGTTCCCAAGCAATTCAAGACCCAGCAATACTACAACGTCTCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCCGGGGACCTTGCTCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGCTCCAATACAACAGCAGTTCCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACCTCGGGGACAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCAACCCCTGTACCATTTGCCGTGGGTTCCTGGCAG
 GCACAATGATGTGCTGATGTACGGTGCCACCTCATCTGGCTCTCCCATCTCAATGGC
 AAGAAGGCACTGGAGGCCATCAGCAGAGAGAGAGGCACCTTCTGTATGGTACCCCCAGCAT
 GTTCGTGGACATTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCATTGCTGGGTCCCTGCACTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGCCTGGTGGTTGCTTATGGAACCAAGAGAACAGTCCCGTGACATTTCGCGCACTT
 CCCTGAGGCACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATTATGCCTCACACGGAGG
 CCCGGATCATGAACATGGAGGCAGGGACGCTGGCAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAAGTGGTATTGGACAGGAGATGTGCCACAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTGTGCTGCAATTCGGCTGAAGGACGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTCACAAATCAACCCCTCACCATTTCAGGAAAGATCCAGAAATTCAACTTCGAGA
 GCAGATGGAACGACATCTAAATCTGTGAATAAAGCAGCAGGCGCTGTCTGGCCGGTGGCCTT
 GACTCTCTCCTGTGAGAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCCAGTTTC
 TGAGCCAGGCACATCAAAATGTCAAGGAATTGACTGAACGAACTAAGAGCTCTGGATGGGTC
 CGGGAATCGCTGGGCACAAGGTGCCAAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCACATTCCTCTGTCTGTCTTGTGATTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGMLRLGRLCAGSSGVLGARAALSRSWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETTAQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVFPKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGLTLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQFTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPVTFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKVGRSKDMIIRGENIYPAELEDFHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCCTGGCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCCCACGATGTTCGTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTCGCGCACTTCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTGCCAC

FIGURE 124

GAGCAGGACGGAGGCCATGGACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGTCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGC GCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTCTCGCTGGC
 AGTGC GGGGTTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCTTGGATCTTCAACGGC
 TTCTGGCGTTTATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGCATACCGCCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCGGCTCGTGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTACCTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTACGCTCAGTGGCTCCTGTGTCCAGGGGTCCCGCTGTAACT
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTGTCCGGCTGCCCCCT
 CCAGAGCCACGACTGTGGCCTCAACCACATCTGTCAACACTTCTACCTCGGCCCCAGTGAG
 ACCCACATCCACCACCAAAACCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCCTCCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCCGCTGGCCACCAGGAC
 CGCAGCAATTGAGGGCAGTATCCTGCAAAAGGGGGGCCCCAGCAGCCCCATAATAAGGCTG
 TGTGGCTCCCAAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTGTT
GAGCTTCTCCACCTGGAAATTTCCCTCTACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCCTGTTCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACTTCCC
 CAGTATCCCCAGCTTCTGTGCGCTGGTTTTGCGGCTTTGGGAAATAAAATACCGTTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCACTCTAAGCACTGCCTCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCGGTAC
 CCAATTGCGCCTATAGTGAGTCGA

MDPARKAGAQAAMIWTAGWLLLLLLRGGAAQALECYSCVQKADDDGCSPNKMKTVKCAPGV DVCT
EAVGAVETIHGQFSLAVRGCSSGLPGKNDRGLDLHGLLAFIQLQQAQDRCAKLNLT SRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPVVSCYNASHVYKGCDFGNVLT TAANVTV
SLPVRGCVQDEFCTRDGVTPGGFTLSSGCCQSRGCSNDLRNKTYFSPRIPLVRLP PPEPTT
VASTT SVTTSAPFVRTSTTKMPAATSQTGRQVEHEASRDEEPRLTGGAAGHQDRSNSG
QYPAKGGQQPQHKNKGCVAPTAGLAALLLVAAGVLL

FIGURE 126

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FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPAPGDEEAQVENLITANATEPQKQRTVEVQPSGGSLWNLRRLLEPLDANVDA

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AAACTTGACGCCATGCAGATCCCGGTCCTTCTCGCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCAGGGAGCCACCCTGGGTGGTCTCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCTCTGAAATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCTCGAACTGGCAGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
CTTCAACTGGGATGCCTTTCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCAGT
GCAACTGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGTGATTTCAACCTACCATAACT
CTTTCCTGACCTCAGGAATCCAATAAAACATTTTCCATCCAA

FIGURE 130

CAGTTCGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCAGGTTGTTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTGTGTAAAGTATTTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTTGACTTGAGAAAAGTGCCCTTCTGCAGCTTCATTGATTTTGTATC
TTCATATTAATGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTCTT
AAAAGTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

FIGURE 132

GGGGAATCTGCAGTAGGTCTGCCGCGCATGAGTAGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCTCTGCCCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCTTTGGAGAATTACGAACCATGTTCAAGTCAAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGGTCCTTGGACGGTGGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGAAGAAAGAAAACCTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTCTTCTGTCTCGGAAAACCCAAAACCTGTTGATGCAGAATACACCAAAAAC
 CAGGCCCTGGAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAAATACAAGTATCTGTTAATTTTCGAGGCGTAGTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAACAGATCTCTCCAATGTCCA
 AGAGCTGTACAAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATTCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAATGTTGAAAACGAACTATAGTAGTCATCATAGGACCATAGTCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACACTGATATGAAGCAGTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTCATTTTCTTAAGACCAATC
 ACAGCTTGTGCTCAGATCATCCACCTGTGTGAGTCCATCAGTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCATTTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTAATCAAGGCGTGATCTCTGTCACTTTATTTAATGTAGG
 AAACCCATGGGGTTTATGAAAAATACTTGGGGATCATTCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTGTAAAACCATAAATCTGTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATTGCATGAGTAATTATTGCAATTGGATT
 TCAGGTTCCCTTTTTGTGCCTTCATGCCCTACTTCTTAATGCCTCTCTAAAGCCAA

MEWASSPLRLWLLFLPLPSAQGRQKESGSKWKVFDIQINRSLNENYEPCCSSQNCSCYHGVE
EDLTPFRGGISRKMAEVRRLKLGTHYQITKNRLYRENDCMFPRSCEVHEHFILEVIGRLPD
MEMVINVRDYPQVPKWEPAIPVFSFKTSEYHDIIMYPAWTFWEGGPAVWPIYPTGLGRWDL
FREDLVRSAAQWPWKKNSTAYFRGSRTSPERDPLILLSRKNPKLVDAEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLNFNRGVAASFRFKHLFLCGSLVFHVGDWLEFFYPQLKPWVH
YIPVKTLNSNVQELLQFVKKANDDVAQEIAERGSQFIRNHLQMDDITCYWENLLSEYSKFLSY
NVRTRKSGYDOII PKMLKTEL

FIGURE 134

CACCCCTCCATTTCTCGCCATGGCCCTGCACTGCTCCTGATCCCTGCTGCCCTCGCCTCTT
 TCATCCTGGCCTTTGGCACC GGAGTGGAGTTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
 GGAGGGATCCCGAGTCTGGTGGTCCGGATGCCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
 CCGCAGCATCCTTGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTGTGGGCAGC
 ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGTACTTTGGGGTCTTCAG
 AGGTCACTGTATGTGGCCTGCCTGCCCCTGGCCTTGCACTGGTGTGTCGGTACTGGGAGCC
 CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCG
 TCCTCTGCTTTGTGCTCCATGTCATCTCCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
 GACTATGCTGAGCTCATGGGCCCTCAAACAGGTATACTACCATGTGCTGGGGCTGGGCGAGCC
 TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTCTTCTCCACCTGCGCCACCCAGTGTGTG
 TGGAGCTGCTGACAGTGTGTTGGGTGGTGCCCTACCTGGGCACGGACCGTCTCCTCCTTGCT
 TTCTCCTTACCCTCTACCTGGGCCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
 CCGGGCCAGCTACAAGAAAACTCCACCTGCTCTCTCGGCCCCAGGATGGGGAGGCAGAGT
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCTCTCCACTGAATTCTAAATCCTTAAAC
 ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAAATCCATGGACTGAAGGAGATGCCCTT
 CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCCCTAAATTTCTGAGTTTCAGCCA
 CTGAACCTCCAAGGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
 TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
 CTGACCACTCCCCCTGGCACTGTTACTTGGCTCTGCGCCTCAGGGGTCCCTTCTGCACCGCT
 GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTCATAGCTGTCCCTCCA
 GGCCCCAACCTTGCCCTCACCCTCCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCTCT
 GGGCTCAGACCCCAACCTAGTCAAGGGGATTCTCCTGCTCTTAACCTCGATGACTTGGGGCTC
 CCGCTCTCTCCGAGGAAGATGCTCTGCAGGAAAATAAAGTCAGCCTTTTCTAAAAAAA

FIGURE 135

MAPALLLI PAALASFILAFGTGVEFVRFTSLRPLLGGIPESGGPDARQGWL AALQDRSILAP
LAWDLGLLLLFVGQHSIMAAERVKAWTSRYFGVLQRSLYVACTALALQLVMRYWEPI PKGPV
LWEARAEPWATWVPLLCFVLHVISWLLIFSILLVFDYAELMGLKQVYHVLGLGEPLALKSP
RALRLFSHLRHPVCVELLTVLWVPTLGTDRLLLAFLTLYLGLAHGLDQQDLRYLRAQLQR
KLHLLSRPQDGEAE

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAGCATGGAATACAGAAAACAACAAAAAAGCTTAAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCTGAGTGTAAGAACCTTCGGCTCGCGTGCTCTG
 AGCTGCTGTGGATGGCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAAATGGAGCCTCTCTGCTGCTGCTACTCTGAGTTTCTTTGTGATGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAAGTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTTGGTGGGGATATGAGTTTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAGGAAGACAAATGTTGGCATTGTCTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAAACCATTAGGC
 ATTCAGGTGGGTAAGTGAAGTTTTGCCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCCTCAGAGAAGTTT
 TTCACAGGTTATCTCTTAATTGATAATTATTCCTATAGAGGATTTTACAAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTTCAAGGTGTTCCCTGCATCTGAGTGGGTGGGTTATATATA
 TGTCCAGAGATTGTGTCGAAGGATCTATGAAATGATGGGTACGTAACCAACCCATCAAGTTT
 GAAGATGTTTATGTGCGGATCTGTTTGAATTTATTAAGTGAACATTTCATATTCAGAAAGA
 CACAAATCTTTTCTTCTATATAGAATCCATTGGATGTCTGTCACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCAAGGAGATCATCACTTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTAAGTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTTGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAATAATTCATGGGAGGTGAGTGTGCTGCGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGTTTACACTGTGATTTATTAGTC
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATATAAGGAATTGGAGGTTTTTGCTAAA
 GAAATTAATAGGACCAACAATTTGGACATGTCATTCTGTAGACTAGAAATTTCTTAAAGGG
 TGTACTGAGTTATAAGCTCACTAGGCTGTAACCAACCAATGTAGAGTTTTATTTATTG
 AACAATGTAGTCACTTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAAAGTCTTCTCACTGAAGTTATACTGAACAAAAATTTTACCTGTTTT
 TGGTCATTATAAAGTACTTCAAGATGTTGCAGTATTTACAGTTTATTTATTTAAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAGGATAGTGAAT
 CATCTTTACATGCAAAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAATGTAAGTCAATAGGTCATTTATGTCATACGTAATCTCTTGGACTTTGTTAAAT
 ATTTTACTGTGGTAATATAGAGAAGAATTAAGCAAGAAAAATCTGAAA

FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGCATGAAGTTCAACAATTGCTCTTGGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACAACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGCTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACCGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAAATT
TTTCTCTACTAGTTATGTTTGATTTCTTTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIIVFAGLLGVFLAPALANYININVDDNNNAGSGQQSVSVNNEHNVANVDNNNGWDSWNS
 IWDYNGNFAATRLFQKKTIVHKMNKEVMPSIQSLDALVKEKKLGKGPGGPPPKGLMYSVN
 PNKVDLDSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

FIGURE 140

CATTCTGAAACTAATCGTGTCTGAGAAATGACTTTGAAAAGCATTGCTTTTTACAGAAGTATA
 TTAACTTTTTAGGAGTAATTTCTAGTTTGGATTGTAATATGAAATAATTTAAAAGGGCTTCG
 CTCATATATAGGAAAATCGCATATGGTCTAGTATTAAATCTTATTGCTTACTGATTTTTT
 TGAGTTAAGAGTTGTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
 GAATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTTGTGTACATG
 CAAGCTTATAGTTGAAATATTTTTCAGGAATTAC**ATGA**ATGACAGTCTTCGAACCAATGTGT
 TTGTTTCGATTTCAACCAGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
 CAGATTCGGTTGCCAACTCGTCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAAT
 CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
 TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCAAATTAAAGCAAAGGGA
 TTGAATCCGGATGGAACCTCCAGCCCTTCAACCCTGGGTGGATTTTCTCCAGCCTCCAAGCC
 ATCATCACCAAGAGAAGTAAAAGCTGAAGAGAAATCACCAATCTCCATTAATGTGAAGACAG
 TCAAAAAAGAACCTGAGGATAGACAACAGGCTTCCAAAAGCCCTTACAATGGTGTAAAGAAA
 GACAGCAAGAGAAGTAGAAATAGCAGAAGTGCAAGTTCGATCGAGGTCAAGAACACGATCACG
 TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
 GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
 GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
 TCATAAAAGGAAAAAATCTCGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
 CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
 GAGAGGTCCCATAAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGACTTTCTCTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
 ATGGACTCAATCAAAACATTAAACGCAAACCTGATTAGGATTTGATTCTTGAACCCCTCTA
 GGTCTCTAGAACTGAGGACAGTTTCTTTTGAAGAAGTATGTTAATTTTTTGCACATT
 AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATGTACTTTATTATAGT
 TGTGTATTGTTATTGCTATAAGAACTGGAGCGTGAATTCGTAAAAATGTATCTTATTTTT
 ATACAGATAAAATTGCAGACACTGTTCTATTAAAGTGGTTATTGTTTAAATGATGGTGAAT
 ACTTCTTAAACACTGGTTTGTCTGCATGTGTAAGATTTTTACAAGGAAATAAAATACAAAT
 CTTGTTTTTTCTAAAAAAGG

FIGURE 141

MNDSLRTNVFVRFQPETIACACIYLAARALQIPLPTRPHWFLLFGTTEEEIQEICIETLRLY
TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
NRRSRSGTYSSRSRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRKKSRSRSQ
SKSRDHSDAAKKRRHERGHHRDRRERSRSFERSHKSKHHGGSRSRSGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATATTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTTAGAGTAATTTCTAGTTTGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTTACATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCACTACCTTGCAGNTAGAGCACTTCA
GATTCCGTTGCCAACTNGTCCCCATTGGTTTCTTCTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAAGCAAAGGGATT
GAATCCGGATGGAATCCAGCCCTTTCAACCCTGGGTGGATTTTCTCC

FIGURE 143

GGCACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGACACGCGTTCTCGCACGCGTC**ATGGC**
 GGTCTCGGAGTACAGCTGGTGGTGACCCTGCTCACTGCCACCCCTCATGCACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTTTGTTCGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGAAAGAGCGGTG
 GGCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCGTTCCAGCTGG
 AGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCACTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTTCTGCTGCTGGCCATGCTGGTGCAAGTGGTGGC
 GGAGGAGACCCTCGAGCTGGGCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAATCTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCAGGCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGGAGACAGACCCATGCTGCAGTTCTTCTCTGC
 ACACAGCTTCTGTCTCCCTGTTTATCCTGTGGCTCTGGACAAAGCCATTGCACGGGAC
 TTCTTGCAACGAGCCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGCGCCTCTGGTTGTCTGGTGGTGGCTGTCCTGCTGCGGCTGGCGGTGACCCGGCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCACTACCTGACGCCGCTCATCCTCACCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGCGCTGGGCCAGCTCCTTACTATCCCCGACCCATCCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCCTGCTTACTCCCTCTTCTCCGTGGCGTCTGCGCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTCGCCAGCCTTTTCGGCCTTACTTCCACCAGCACTTGGCA
 GGCTCT**TAGC**TGCCTGCAGACCCCTCCTGGGGCCCTGAGGTCTGTTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCCCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGGTTCCCTTACCCACAGTGCTGACCCGCGGCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGAAGTGGCAGGGTGATGCTGGCTGCTCTTCTGAACAAATAAGGAGCATGCC
 GATTTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLTVTRLYFSAEEGERSVCLTFAFLFLLAMLVQV
VREETLELGLEPGLASMTQNLEPLLKKQGDWALPVAKLAIRVGLAVVGSVLGAFILTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLR LAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVSLQYLTPLIILTNLCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWTTAACQLLASLFGLYFHQHLGS

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FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
TGTTCCGATACAAGCACCCGINTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
CAGAGGCAGGAAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTT
CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCTGCTGCTGGC
CATGCTGGTGCAAGCG

FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAACTGGCTT
 AATCTGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGATGGCAAGGTTTGGCTTAAAGGAGC
 TTGGCTGGTTTGGGCCCTTTGTAGCTGACAGAAGGTGGCCAGGAGAATGCACACACTGCTCGGAGAATGAAGG
 CGCTTCTGTTGCTGGTCTTGCTTTGGCTCAGTCTTGCTAACTACATGACAAATGTGGGCAACCTGCACTTCTGT
 TATTGAGAACTCTGTAAGGTGCTCCCACTACGGCCTGACCAAGATAGGAAGAGGCGCTCACAAGATGGCTG
 TCCAGACGGCTGTGCGAGCTCAGACGCCAGGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGAGAGGCTTGGCTTAGCAACCTTGCCTAGCTGTCTCGGCAGAGGACGGGCGAGCAATCAGCCCA
 GTGGACTTGGCCGGAGCAACCGAATAGGCGACGGCCCTTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAATAAAATCGAGCTTTGAGTGTCTTCGAAGGACAAAGAGCGGAGTGCAGTTGCCAACCATCGCCGACCAAG
 GCAGGAAAAATCTGAAAACACCACTGCCCTGAAGTCTTTCCAAAGGTTGTACCACTGATTCCAGATGGTGAA
 ATTACCAAGCATCAAGATCAATCGAGTAGATCCAGTGAAGGCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCGCTACTGCCAG
 GAGACATCATTTCAAAGGTCACCGGATGGACATCAGCAATGTCCCTCACAACCTAGCGTGTGGCTTCTCTGCGG
 CAGCCCTCGCAGTCTGTGGCTGACTGTGATGCGTGAAACAGAAATTCGCCAGCAGGAACATGGACAGGCCCC
 GGATGCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAAACCTGGTGGCAAGGTGGATGAGCCTTGGGGTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTTAGCCATCAATGGACATGATCTTCGATATGGCAGCCCAAGAA
 TGCGGCTCATCTGATTTCAGGGCAGTGAAGACGTGTTCACTCTGCTGTTCCCGCAGGTTTCGGCAGCGGAGCC
 CTGACATCTTTTCAGGAAGCCGGCTGGAAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACT
 CCCAACCCCTCCATCCTCAATTACTTTGTATGAGAAGTGGTAAATATCCAAAAAGACCCGGTGAATCTCT
 CGGCATGACCGTCGACAGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTATCAGTGTGTAGGCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAACAGGTGACATTTTGTGAATGTGGATGGGCTCGAACTGACA
 GAGGTGACGCGGAGTGAGGCACTGGCATTTATTGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGAGTATGAGCCCGAGGAAGCTGCAGCAGCCAGCAGCCCTGGACTCCAACCAACATGGCCCCACCCA
 GTGACTGGTCCCCATCTGGGTCATGTGGCTGGAATTACCACGGTGCTGTATAACTGTAAAGATATGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGTAGAGGTTATGAAGAATACAATGGAACAAACCTTT
 TTTTCATCAATCCATTGTTGAAGGAACACCAAGCATCAATGATGGAAGAATTAGATGTGGTGATATTCTTCTG
 CTGTCATGGTAGAAGTACATCAGGAATGATACATGCTTGTCTGGCAAGACTGCTGAAAGAACTTAAAGGAGA
 ATTACTCTAACTATTGTTTCTTGGCCTGGCACTTTTTATAGAAATCAATGATGGGTGAGAGGAAAAACAGAAAA
 TCACAAATAGGCTAAGAAGTTGAAACACTATATTTATCTTGTGAGTTTATATTTAAAGAAAGAAATCAATGT
 AAAAATCTCAGGAAAGTATGATCATCTAATGAAAGCCAGTTACACCTCAGAAAAATGATTCCAAAAAATTA
 AAACCTACTAGTTTTTTTTAGTGTGGAGGATTTCTCATTACTACAACTTTGTTATATTTTCTTATTTCAAT
 AAAAGCCCTAAAACACTAAATGATTGATTTGTATACCCCACTGAATTCAGCTGATTAAATTTAAATTT
 GGTATATGCTGAAGTCTGCCAAGGTACATTATGGCCATTTTTAATTTACAGCAAAATATTTTTTAAATGCA
 TTGCTGAGAAGCTGCTTTTCATCAACAAAGAAATAATTTTTTCAGAAGTAAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGCPCDGCASLTAT
APSPEVSAAAATISLMTDEPGLDNPAYVSSAEDGQPAISPVDSGRSNRTRARPFERSTIRSR
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAPAEVFPRLYHLIPDGEITSIKINRVDP
SELSIRLVGGSETPLVHIIIQHIYRDGVIARDGRLLPGDIIKLVNGMDISNVPNHVAVRLL
RQPCQVLWLTVMREQFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLVKRVDEPGV
FIFNVLDGGVAYRHHGQLEENDRVLAINGHDLRYGSPESAHLIQASERRVHLVVSQRQVRQS
PDI FQEAGWNSNGSWSFGPGERSNTPKPLHPTITCHEKVNNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTGDILLNV DGV ELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPFPIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGR
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTTACTTTACTCCAGCACCTTCCTCTCCCAGGCAAATGGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCCTGCTTGGGTAC
CCATTGAGAAACTCTGCAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCCGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTGATGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTTCTTTCCCAATGCCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

MKILVAFVLVLTIFGIIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
 IFDYKHGYIASRVLRRACFILKMDHQNIPTLNNLQWYIYEKQALDNMFMSNKYTWVKYNPLE
 SLIKDVDWFLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAGLGLGILGISICADIHV

FIGURE 150

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCCAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGGCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCTGGAAGTTTCCCAAAG
GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACCACCGCCCATCACCTATTCCCTC
TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGGTGGTGAAGACCCACGAGCCGGCCTCCTT
CAACCTCAACGTCACACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCTT
CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
CCAGTGTCTGAGCTGCGGGCCAACCTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
GATGATCTGCCAGGCGTCTCGGGCAGCCACCTATCACCAACAGCCTGATCGGGAAGGATG
GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAATCTCTCCTTCTGCCG
AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAACAACGCCAATGTCCAGCACAGCGC
CCTCACAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCTTGGAGA
GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGTCTGAGTGAAGAGGAGTTTGGG
GGGTTCAGGATAGGGAATGGGGAGGTGAGGAGCGCAAAGCAGCAGCCATG**TAG**AATGAACC
GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTCTGTAATTTGGA
GTTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTTGCCACAAAAAAAAAAAAAAAAAAAAA

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG). The subjects were divided into two groups: the control group (CG) and the experimental group (EG). The CG was divided into two subgroups: the control group (CG) and the control group (CG). The EG was divided into two subgroups: the experimental group (EG) and the experimental group (EG).

FIGURE 151

MGLPLGLFCLAVLAASSFSKAREEEITPVVSIAYKVLEVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVKTHEPASFNLVTLKSSPDLTYFCRASSTSGAHVDSARLQMHWELWSK
FVSELNANFTLQDRGAGPRVEMICQASSGSPPITNSLIGKDGQVHLQQRPCRQPANFSEFLP
SQTSDFWFCQAAANNANVQHSALTVPVPGGDQKMEDWQGPLESPILALPLYSTRRLSEEEFG
FGRIGNGEVGRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCTCACCTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGA
 CTTTCTTCTCACTATGACTGTGGCAACAAGACAGTCAACCTGTCACTCCCCTGGGGAAGAAA
 CTAATGTCAACAACGGCCTGGAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGTC
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCCTCATCTTTGCTGCCTCCTCATCATCTCCCTGCTTCATCTCCTTGGA
 TCTGAGGAGAGTCCTTTAGAGTGACAGGTTAAAGCTGATACAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAACCTCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCAGT
 GGCCCTCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCCT
 TTGCCAACAAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACCTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTC
 TCTTTTGTGGAAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGATTCTTTCCGTGCTCTGAAAGAG
 AATTTTTAAATTATTTAATAAGAAAAAATTTATATTAATGATTGTTTCCCTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCATTTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCQVGGQVDEKTFLL
HYDCGNKTVTPVSPGLGKKNVTTAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCTCACAATTTTCATTCTGTTTCTGACTTTCAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTCTTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAACCTCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATGAGAATTGTCGTGCTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCTGTAT
CATCCTTTTCAATAAACTGTATTCATTTTGAIAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTQHFWARL

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FIGURE 156

GTTCTCCTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAAGTGTGCACCACCACACCTGGAATGCCATCCTGCTCCCGTTCGTCTA
 CCTCACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGCTCAGCCGGGGCCCC
 AGAACTGCCCCCTCCGTTTGTCTCGTGCAATAACCAAGTTCAGCAAGGTGGTGTGCACGCCCGG
 GGCTCTCCGAGGTCCCGCAGGGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCCGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCGAGT
 TGGGCAGGAACCTCCATCCCGCAGATTGAGGTGGGGGCCCTTCAACGGCCTGGCCAGGCTCAAC
 ACCCTGGAGCTGTTGCACAACCTGGCTGACAGTCATCCCTAGCGGGGCCCTTTGAATACCTGTC
 CAAGCTCGGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCCTCTTACGCCCTCA
 ACCGGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAACCTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCCCTGGTGGGGCTGGAGGAGCTGGAGATGTCAAGGAACCACT
 TCCCTGAGATCAGGCCCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTGATG
 AACTCACAGGTGAGCCTGATTGAGCGGAATGCTTTTGACGGGCTGGCTTCACTTGTGGAAC
 CAACTTGGCCCAACAATAACCTCTCTTCTTTGCCCATGACCTCTTACCCTGGTGGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATTCGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCACCAATTCCACCTGCTGTGGCCGCTGTCATGTCTCCAT
 GCACATGCGAGGCCGCTACCTCGTGGAGGTGGACCAGGCCCTCCTTCCAGTGTCTGCCCCCT
 TCATCATGGACGCACTCGAGACCTCAACATTTCTGAGGGTCGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCCCTCGGTGAAGTGGTTGCTGCCCAATGGGACAGTGTCTCAGCCAGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAACCTTTCCACGCTGCTGC
 TTTGACACTGGGGGTACACATGCATGGTGACCAATGTTGCAGGCCAATCCAAACGCTTCG
 GCCTACCTCAATGTGAGCAGCGCTGAGCTTAACACCTCCAACCTACAGCTTCTTACCACAGT
 AACAGTGGAGACCACGAGATCTCGCCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCAGTCCACTGGTTACAGCCGCGCATATACCACCTTACCACGGTGTCTTACAGACTACC
 CGTGTGCCCCAAGCAGGTGGCAGTACCCGCGACAGACCACTGACAAGATGCAGACCAGCCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCCATGTTGATTGTCTTCTATAAACTTCGTAAAGCGCACAGCAGCGGAGTACAGTC
 ACAGCCGCCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCCGGTGATCAGGTGAGGGGGCAGTAGTGCTGCCCAAAATTC
 ATGACCATATTAACATAACACCTACAAACCAGCACATGGGGCCCACTGGACAGAAAACAGC
 CTGGGGAACCTCTGTGACCCCCACAGTCACCACATCTCTGAACCTTATATAATTACAGACCCA
 TACCAGGACAAAGGTACAGGAAACTCAAATA**TGAC**TCCCTCCCCCAAAAACTTATAAAAT
 GCATAGATGCACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTA
 TATGCTTATATATTAAGTCTATGGGCTGGTTAAAAAAAACAGATTATATTAATAATTAAAGA
 CAAAAGTCAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLNFKYLNLMCNKIDMPNLTPLVGLLEELEMSGNHFFPEIRPGSFHGLSSLKKLW
VMNSQVSLIERNAFDGLASLVELNLAHNNLSSLP HDLFTPLRYLVELHLHHPWNCDCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LNTSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDITDKMQTSLDEVMKTKIIIGCFVAVTLLAAAMLIVFYKLRKRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLPTIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTTISEPYIIQTHTKDKVQETQI

[illegible]

MELGCWTLQLGLTFLQQLLISSLPREYTVINEACPGAENWIMCRECCEYDQIEVCVPGKREVV
 GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGFYCAECRAGWYGGD
 CMRCGQVLRAPKGQILLESYPLNAHCWTHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
 GDNRDGQIIKRVCGNERPAPIQSIGSSHLVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDG
 TCVLLDKAGSYKCACLAGYTGRQCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKGTV
 VSFFCNNSYVLSGNEKRCTQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLH
 QLYSAAFQKQLKSAPTCKPALPFGDPLMGYQLHHTQLQYECISPFYRRLGSSRRRTLRTGK
 WSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
 RTVVVAACHCVTDLGKVTMIKTADLVVLGKGYRDDRDEKTIQSLQISAIILHPNYDPILLD
 ADIAILKLLDKARISTRVQPICLAASRLDSTSFQESHITVAGWNVLADVRSPGFKNDTLRSG
 VVSVVDSLDCCEEQHEDHGVPSVTDNMFCSAWEPTASDICTAETGGIAAVSPFGRASPEPR
 WHLMGLVSWSYDKTCSHRLSTAFTKVLFPKFDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAGGCTCAACTGA
 AGCTTCTTGCCTGCAGTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACTTTCACCTTTCCTACAAATCCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTAATACTTTCGTTGGGTGCCATTCAAGAGATTCTCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCCTCATTTTGGGGAAGGAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAACTTGACAACTGTCCTTCTGTGTCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCATCTCCTTTGGAAGAGGTACAGGCAGAAAAATC
 CCAAAGTGTCAGAGGCCGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCCT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACCTACTGGGGATGGGAGGCCGAAGACGATGACCTCAGACTCAGGTTGAGCTCCAAAG
 AATGAAAATTTCCCGGCCCTGCCCTGAAGTGGGTAATATACAAATGGTCTTCCACACTAGAG
 ACAAAGGCAATGAGGTGAACGCAGAACGGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTGAGTAGTGTCTTATAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTCTGGTTTGGTGCA~~TGA~~CCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGCTGATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTGTTGAGCTGAATTTTCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAAACAGTTGTAACAAGACAGCTTCTTAGTCATTTTGTATG
 AGGGTTAAATATTGTAATATGGATACTTGAAGGACTTTATATAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAAATAAGACTGCTGAATGTCTGAGAGAACCAGAGTTGTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTATCATTATCTGTACAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGCTGCAAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACAGAGAATACATCTCTATTAGTTTTTAAAGAGTTTTTGTAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAAAATGTGAAAAAGCAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLCLTVVGWATSNYFVGAIQEIPKAKEFMANFHKTLILGKGKT
LTNEASTKKVELDNCPSVSPYLRGQSKLIFKPDLTLEEVQAENPKVSRGRYRPQECKALQRV
AILVPHRNREKHLMYLLEHLHPFLQRQQLDYGIIYVIHQAEKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVG RNSTGYRLRYSGYFGGVTALSREQFFKVNG
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGKYTMVFHTRDKGNEVNAERMKLLHQVSR
VWRTDGLSSCSYKLVSV EHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCTGCGCAGCGGGCTGTGGGCGCGCCCGGAGGAGCGACCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCGCTCCGGGCCCCGCAATG
 GCCCAGGAGCTGTGGTTCGCGCTCGGCCCGCATCCTCTGGCTTGCTGCTCCTGCCCTGGGC
 CCGGCGAGGGGTGGCCGAGGCTGTATGAATCAATCTCACCACCGATAGCCCTGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGAGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCGCGG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCCTCCCATCACAGAGTTCTCTCGTGGGGACCTTGTGTCAACCAGAACACTTCCCTACC
 CTGGCCAGCTCCTATCTACTAAGACCGTCTGAAAGTCTCCTTCTCCTCCACGACCCGA
 GCAACTTCTCAAGACCGCTTGTTTCTCTACAGCTGGGACTTCGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCATCATCGGGACCTTACCCTGAAGCT
 CAAAGTGGTGGCGGAGTGGGAAGAGGTGGAGCCGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCTCGCTGAAGCTGCAGGAACCCCTTCGAGGCACTCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 CTGACTGTGTGTGGCGTCTCAAGCCTGAGTGCTCCCGCTGGAGGAAGGGGAGTGCCACC
 TGTGTCCGTGGCCAGCAGCGTACAACCTGACCCACACCTTCAGGGACCTGGGGACTAC
 TGCTTCAGCATCCGGGCCGAGAATATCATCAGCAAGACACATCAGTACCACAAGATCCAGGT
 GTGGCCCTCCAGAAATCCAGCCGGCTGTCTTGTCTTCCCATGTGCTACACTTATCACTGTGA
 TGTGTGGCTTATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACC CGAGCCACCTCTGGGGTCAGGTGCTGCTGCCAGATGTGCTGTGGGCTTTCTTGTCT
 GGAGACTCCATCTGAGTACCTGGAATTGTTCGTGAGAACCACGGGCTGCTCCGCCCTCT
 ATAAGTCTGTCAAACTTACACCGTGTGAGCACTCCCGCTCCCGACCCCATCTCAGTGTAA
 CTGACTGCTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACAGGAGGGGTTTCATT
 TGCCTGGGGCTGTTGGCTGGATCATCCATCCATCTGTACAGTTACGCCACTGCCACAAGCC
 CCTCCCTCTCTGTACCCCTGACCCAGCCATTACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCACTCGGTTACCAACCCCTTGACCCCTACCTTTGAAGAGGCTTCGTGCAAGACT
 TTGATGCTTGGGGTGTCCGTGTTGACTCCTAGGTGGGCTGGCTGCCACTGCCCCATTCTCT
 CTCATATTGGCAGATCTGCTGTCCATTGGGGGTTCTCAGTTTCTCTCCCGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAAGAGGTCTATAAAGGGTTAAAAATCATTAACCTAAAGTTGTAC
 ACATAGATGGGCACACTCACAGAGAGAAGTGTGCATGTACACACACCACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTTCAGATGATCAGCTCTGTA
 TCTGTTAAGTTCGGTTGCTGGGATGCACCTGCACATAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCCGGGCCCTCCCTTTGTGCTTTGTCTCTGCAGTTCTTGC
 GCCCTTTATAAGCCATCCTAGTCCCTGCTGGCTGGCAGGGGCCCTGGATGGGGGGCAGACT
 AATAGCTGAGTGATTGCAGAGTGCTTTATAAATATCACCTTATTTTATCGAAACCCATCTGTG
 AAATCTTCACTGAGGAAAAGGCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCCGGGCGGG
 TGGCTACGCGCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGTTGATCAGAGATCAGGA
 GATCGAGACCACCTTGCTAACACGGTGAAACCCCGTCTCTACTAAAAAATACAAAAGTT
 AGCCGGGCTGTGGTGGGTGCCTGTAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAATG
 GTGCCAACC CGGAGCGGAGCTTGCAGTGAGCCAGATGGCGCCACTGCATCCAGCTGGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGGEFPVSVWVTAADCWMCQPVARGF
VVLPITEFLVGDVVTQNTSLPWPSYLTKTVLKVSFLLHDPNSFLKTALFLYSWDFGDGTQ
MVTEDSVVYYNYSIIIGTFTVKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
GPTLIQTFQKMTVTNLFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
YCFsIRAENIISKTHQYHKIQVWPSRIQPAVFAPPCATLITVMLAFIMYMTLRNATQQKDMV
ENPEPPSGVRCCQMCCGPFLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

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FIGURE 165

MALSSQIWAACLLLLLLASLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

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FIGURE 166

CTGTGAGGAAGGACCATCTGAAGGCTGCAATTGTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACCATGTTCTCTGTTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTTCACCTCCTTCTCGTTTTTCATCATAGTGCCAGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAAGTCTGTTAAAAATCTTTGCGTGGGCTA
 CTTTGAGAAATGGAGCGAGGACCCAGGAGAAGAACCCAGCTTTACAAGCCCTACACCAAC
 GGAATCATTGCAAGGATCCCACCTTCACTAGAAGAAGAGATCAAAGAGATTTCGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTTCTACTTTTTGCC
 GGAAAGGAATGGAGACCATTATGGATGATGAGGTGACAAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTGTGGGGGTTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCGCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACCTGTGGTGGGATACTTGCACAAAT
 GGGAGGTTTAAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTTACCGGATCTGCGTGC
 AGCGCTGACAGCCATCATCACTACCATGACAGGGAAAAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAATCATACCTCACCGATCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGACCGGGGACTCATGGGTGTGATTACAGAGAGCCATGGTGAAGGCCTG
 CCCACACGTCTGGTTTGGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATTCTCTCTTCCCAGAGAAGAACTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATGGAGCCACAGTTTACCC
 TGTGTCTATCAAGTATGACCTCAATTTGGCGATGCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCCATTGTCTGCAGCGTGTGGTACCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGCGAATAGGGTGAATCTGC
 CATTGCCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAAGCCAC
 AAGGACAGGAGCGCTCCCTGAAGCCTGCCCTCCAGCTGGCTGGGGCCACCGTGC GGGGTGC
 CGGGCTCAGAGCTGGAGTTGCCGCGCGCCGCCCTCACTGCTGTGCTCTTCCAGACTCCAGGG
 CTCCCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCCTTGGTGGTCTAAACCGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCCCTTGTCTTTTACAATAAGTCTGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CTTTTCACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGCCTGACAAGAGTCTGTTATGCAAGCCGCTGTGCCAGGATGTGCTGGGGCGGCCACCCG
 CTCTCCAGGAAGGCCACAGCTGAGGCCTGTGGCTGGCTTCGGCCTCAACATCGCCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTATCTGCAGGGGCTTTCAGCAAAATG
 AAGGTTAGATTGTTTATGCTGCTGATGGGGTTACTAAAGGAGGGGGAAGGCCAGGTG
 GGCGCTGACTGGGCCATGGGGAGAACGTGTGTTCTGCTACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTGTGTAATGTGTCTCGGTTTCCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTATTCTACCTCACAGGGCTGTTGTGGGGATTAAGTGCTGCGGGTGAGTGA
 AGGACACATCAGCTTCAGTGTTCAGGTACAGGCCACAAAACGGGGCAGCGCAGGCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFD₁SLIVNLLGISLT₂VLFTLLLVFIIVPAIFGV₃SFGIRKLYMKSLLKIFAWATLRME
RGAKEKNHQLYKPYTNGIIAKDPTSLEE₄EIKEIRRS₅GSSKALDNTPEFELS₆DI₇FYFCRKGME
TIMDDEVTKRFSAEEL₈ESWNLLSRTN₉YNFQYISRL₁₀TLVLWGLGVLIRYCFL₁₁LP₁₂LRIALAF₁₃TG
ISLLVVGTTVVG₁₄YLPNGR₁₅FK₁₆EFMSKHVHLMCYRICVRALTAI₁₇TYHDREN₁₈RPRNGGIC₁₉VA₂₀NH
TSPIDV₂₁IILASDGY₂₂YAMVGQVHGGLMGV₂₃IQRAMVKACPHV₂₄WFERSEV₂₅KDRHLVAKRLTEHVQ
DKSKLPILIFPEGTCIN₂₆NTSVMMFKKGSFEIGATVYPVAIKYDPQFGDAFWN₂₇SSKYGMV₂₈TYL
LRMMT₂₉SWAIVCSVWYLP₃₀PMTREADEDAVQFANRVKSAIARQGG₃₁LV₃₂LLWDGGLKREKVKDTF
KEEQQKLYSKMIVGNHKDRSRS

FIGURE 168

GCCCTCGAAACCAGGACTCCAGCACCTCTGGTCCCGCCCTCACCCGGACCCCTGGCCCTCA
CGTCTCCTCCAGGGATGGCGCTGGCGGCTTTGATGATCGCCCTCGGCAGCCTCGGCCTCCAC
ACCTGGCAGGCCCAGGCTGTTCCACCATCCTGCCCTGGGCCTGGCTCCAGACACCTTTGA
CGATACCTATGTGGGTTGTGCAGAGGAGATGGAGGAGAAGGCAGCCCCCTGCTAAAGGAGG
AAATGGCCCACCATGCCCTGCTGCGGGAATCCTGGGAGGCAGCCAGGAGACCTGGGAGGAC
AAGCGTCGAGGGCTTACCTTGCCCCCTGGCTTCAAAGCCCAGAATGGAATAGCCATTATGGT
CTACACCAACTCATCGAACACCTTGTACTGGGAGTTGAATCAGGCCGTGCGGACGGGCGGAG
GCTCCCGGAGCTCTACATGAGGCACCTTCCCTTCAAGGCCCTGCATTCTACCTGATCCGG
GCCCTGCAGCTGCTGCGAGGCAGTGGGGGCTGCAGCAGGGGACCTGGGGAGGTGGTGTCCG
AGGTGTGGGCAGCCTTCGCTTTGAACCCAAGAGGCTGGGGGACTCTGTCCGCTTGGGCCAGT
TTGCCTCCAGCTCCCTGGATAAGGCAGTGGCCACAGATTTGGGGAGAAGAGGCGGGGCTGT
GTGTCTGCGCCAGGGGTGCAGCTAGGGTCACAATCTGAGGGGCTCCTCTCTGCCCCCTG
GAAGACTCTGCTCTTGGCCCCCTGGAGAGTTCCAGCTCTCAGGGGTGGGGCCCGTGAAGTCCA
ACATCTGCCACTTAGGAGCCCTGGGAACGGGTGACCTTCATATGACGAAGAGGCACCTCCAG
CAGCCTTGAGAAGCAAGAACATGGTTCGGGACCCAGCCCTAGCAGCCTTCTCCCCAACAGG
ATGTTGGCCTGGGGAGGCCACAGCAGGGCTGAGGGAACCTCTGCTATGTGATGGGGACTTCCT
GGGACAAGCAAGGAAAGTACTGAGGCAGCCACTTGATTGAACGGTGTGCAATGTGGAGACA
TGGAGTTTATTGAGGTAGCTACGTGATTAATGGTATTGCAGTGTGA

FIGURE 169

MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVGCABEMEKAAPLLKEEMAHH
ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSNTLYWELNQAVRTGGGSREL
YMRHFPFKALHFYLIRALQLLRSGGCSRGPGEVVFRGVGSLRFEPKRLGDSVRLGQFASSS
LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTCAGTGGCTGACTTCCAGAGAGCAATATGGCTGGTTCCTCCCAACATGCCTCA
CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
GTCGGTTCCGTTGGTGGGGCCGTGACTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
TATTGTCTGGACCTTCAACACAACCCCTCTTGTACCATAACAGCCAGAAGGGGGCACTATCA
TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCAGATGGAGGCTACTCCCTGAAG
CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
GAACATGGGGAAGAGGATGTGATTATACCTGGAAGGCCCTGGGGCAAGCAGCCAATGAGTC
CCATAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
GCGTTGCCAGGAACCCCTGTGAGCAGAAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
GAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCCTCCTGTGTCTCCTGTTGGTGCCCTT
CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTCTGGGAACTCCTAACATATGCCCCCAT
TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCTAAAGGAAGA
TCCAGCAAATACGGTTTACTCCACTGTGGAAATACCGAAAAAGATGGAAAATCCCCTCAC
TGCTCAGATGCCAGACACCAAGGCTATTGCCTATGAGAATGTTATCTAGACAGCAGTG
CACTCCCCTAAGTCTCTGCTCA

MASSPTCLTIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
IQPEGGTIIVTQNNRNRERVPDGGYSCLKSLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
YEHLSPKPVMTGLQSNKNGTCVTNLTCCEMHGEEDVIYTWKALGQAANESHNGSILPISWRW
GESDMTFICVARNPVSRNFSSPTLARKLCEGAADDPDSMMVLLCLLLVPLLLSLFVLGLFLW
FLKRERQEYIEEKKRVDICRETPNICPHSGENETEYDTPHTNRILKEDPANTVYSTVEIP
KKMENPHSLLTMPDTPRLFAYENVI

FIGURE 172

CTGGTTCCCAACATGCCTCACCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCGGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCACCATAC
AGCCAGAAGGGGGCACTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATATATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCTGTCAGCAGAAACTTCTCAAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCTCCATGGTCTCCTCT
GTGTCTCCTGTTGGTGCCCCCTCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGGGGAA
ACTCCTAACATATGCCCCCATTCTGGAGAGAAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACAAATCCTAAAGGAAGATCCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAA
AGATGGAATAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTTGCCTATGAG
AATGTTATCTAGACAGCAGTGCACTCCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTTGGGACTGACCCTAGTCTGTGTCCATGCAGAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAACGAAAAGGATGGGGA
AACCTTCCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGGCCTGAGCCTCCAGTGTGAGTGGAC
ACTTCTCACCAGGACTCCACCATCATCCCTTCTATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATTCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAT
TTTTCATGAAATATTCTCTTCTCTGTTCAATAAATGATTACCTTGCACTTAA

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FIGURE 174

MKMLLLCLGLTLCVHAEASSTGRNFNVEKINGEWHTIILASDKREKIEEHGNFRLFLEQ
IHVLENSLVLVKVTVRDEECSELSMVADKTEKAGEYSVTYDGENTFTIPKTDYDNFLMAHLI
NEKDGETFQLMGLYGREPDLSDDIKERFAQLCEEHGILRENIIDLSNANRCLQARE

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FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAACCCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAAGTGAATGTTTCTTTTCATCATTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTCATCCAGAATCCTTCAACTTGCAAGTGGTTTTTCAATGACTCTTGTGCACCTCCTACTG
GTTTCAATAAACCCACCAGTAACGACACCATGGCGAGTGGCTGGAGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAAACAAACATAGGCTTATCCACTTCTCAGTATTTTTAGGTCTATTGCT
TGTTGGAATTCTGGAGGTCTGTTTGGGCTCAGTCAGATAGTCATCGGTTTCCTTGGCTGTC
TGTTGGAGTCTCTAAGCGAAGAAGTCAAATTGCTTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAAAAA

MTTCGEGWTSCTNGFSLVLLVLLLVGLVNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATMTSLTARKACCNNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCSNPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGRASSFHF DSEENKRL
IHFSVFLGLLLVGILEVLVFLGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTCGAATCCAAATCACTCATTTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACC**ATG**AGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGTCTACAGGCCCATGCTCTTGTCT
GCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGCAGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGAAA**TAG**TGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

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FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKKRLSLKKSWWK

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FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCCGCCCCAGTGCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGAC**ATG**GAGAGAGTGACCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCCTGTACCTGAGAAGGCCATCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCT**TGA**GCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCAGCACCTCTCCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGCGAGGCTGTTAGGCCCCCTTCTGATCAGGAGGCTTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

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FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDFFYYDWKNLQLSGLICGGLLAIAAGIAAVLSGKCK
YKSSQKQHSFVPEKAIPLITPGSATTC

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGTGCTCCCGACAGAAGGATGTCGCTGCTGAGCCTGCC
 TGGCTGGGCTCAGACCGGTGGCAATGTCCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAACTGCCGCCGGCTCC
 AGTGTTTCCACAGCCCCAAAACGGAAGTGGTTTTGGGGTCACCTGGGCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGCCACCTATTCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGAAGCCCTGG
 CTGGGAGAAGGGATACTGCTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCCATTTCAACATCCTGAAGTCCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGCGCAGCTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGCCAGTGAATATATTTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTTCTGTATTACCTCTCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCCTGGTGATGACTTCACAGAGCTGTCTATCCGGAGCGGCGTCG
 CACCCTCCCCACTCAGGGTATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTGCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTCAGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCAGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACTGTGTGGCCGGATCCTGAGGTCTACGAC
 CCCTTCCGCTTTGACCCAGAGAACAGCAAGGGGAGGTCACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAAGTGCATCGGGCAGGCGTTCGCCATGGCGGAGATGAAAGTGGTCTGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACCTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCTGAATGTAGGCTTGCA
GTCACTTTCTGACCCATCCACCTGTTTTTTTGCAGATTGTCATGAATAAAACGGTGTGTCAAA

MSLSLSLPWLGLRPVAMSPFWLLLLLVGSGWLLARILAWTYAFYNNCRRLQCFQPQPKRNWFEG
HLGLITPTEEGLKDSQMSATYSQGFVTWVGLPIIPFIVLCHPDTIRSI TNASAAIAPKDNLF
IRFLKPWLGE GILLSGGDKWSRHRMLTPAFHFNILKSYITTFNKSANIMLDKWQHLSAEGS
SR LDMFEHISLMTLDSLQKCIFSFDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
LSHDGRRFHHRACRLVHDFTDAVIERRRRLTPTQGIDDFKDKAKSKTLDFIDVLLSKDEEG
KALSDEDI RAEADTFMFGGHDTTASGLSWVLYNLA RHPEYQERCRQEVQELLKDRDPKEIEW
DDLQQLPFLTMCVKESLRLHPPAPFIFRSCTQDIVLPDGRVIPKGITCLIDIGVHNHPVTW
PDPEYVDPRFDENSGKRSPLAFIPFSAGFRNCIGQAFAMAEMKVVV LAMLLHFRFLPDHT
EPRKLEYLIMRAEGGLVL RVEPLNVGLQ

CAACAGAAGCCAAGAAGGAAGCCGCTCTATCTTGTGGCGATCATGTTATAAGCTGGCCTCCTGC
TGTTTGCTTTTTCAGGATTCTTAAATCCTCTCTTATCTCTTCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCTGATTGCTTCTGGAAATACTGTGTCTGAAGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAAAC
AGTGTGGAGAAAAACTAGGCCAACTACACCCTGTTTCATTGTGTACCTGGAAAAATAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAAAA

Figure 1 illustrates the steps of the proposed algorithm for finding the minimum spanning tree of a graph. The graph has 10 nodes and 15 edges. The steps are as follows:

- Initial graph with 10 nodes and 15 edges.
- Selection of edge (1,2) with weight 1.
- Selection of edge (2,3) with weight 1.
- Selection of edge (3,4) with weight 1.
- Selection of edge (4,5) with weight 1.
- Selection of edge (5,6) with weight 1.
- Selection of edge (6,7) with weight 1.
- Selection of edge (7,8) with weight 1.
- Selection of edge (8,9) with weight 1.
- Selection of edge (9,10) with weight 1.
- Selection of edge (1,3) with weight 2.
- Final minimum spanning tree with 9 edges and total weight 9.

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDSDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSSTNIFNPRGNLRKFQDFSGODPNILLSHLLARIWKPKKRETPDCFWKYCV

FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
 GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
 CCACCTCCGCCAGGAACTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
 AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
 CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
 GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCGGAAGATGGAGGTCAAGCAGA
 AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
 CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
 GAAGAGGCCAAAGAGGCCCCAGCCGACAAGTGATGCCCCACAAGCCTTACTCACCTCTCTCT
 AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCACGACTGTTGTA
 CAAGCTCAGGAGCGAATAAATGTTCAAACCTGTA

FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGTCCGCACGGACCCAGATGTCAAGAAT**ATGA**ACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCTGCTGGACTTTCTTGGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGGTGGTCAAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCCCTGAGCCCCCACGCCCTGGGGCCAGAGTCTTT
 GTCCCCGTGTGCGCATGTGTTCAAGGTGAGCCTCTCCAGAAGTGAGATCATGGACAAAAA
 GGGCAAATCACAGGAAGAAATTAAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCT**TGA**AGTAACAAGTTTAAAAATGTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGACATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTTCTAACATGAAATATATTACAGGCAGGTCACCCCTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGT
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTTGGTCATGGTGGGCCAGCTGCAAAAGC
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGGTTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCCTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCACCAAGA
 GCCTCCTTGTTCATAACCACAGGTTACCCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAAATGAAAGTGCAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLLDLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGKSQEEIKSMRTQQ
AQQEAELTPRPAGVVPGA

0996643-11401

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCCTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGTCTGGCAGCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAACTGTGGAAG
 AACCAGGGGAGAGGTGCCGAAGTTTCATTGAACTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCCTCCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCCTGCCTGTGGGCTCAAAC TGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTCTGTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAAGTC
 TTCCAAGCGACTGTCAACTTGGGTCCAGAAGACTGGAGACCACATGTTTGAATTATGGCTG
 GGCTTCTACATGGCCTGGCTCTCCTTCACCTGCTGCATGGCGTGGCTGTCAACACCTTCA
 ACACGTACACCAGGATGGTGCTGGAGTTCAGTGCAAGCATAGTAAAGAGCTTCAAGGAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTTCCCTCGGCGGCTGTCAAGTGCAGCCCCAC
 CGTGGGTCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTAGGAGTTAAGCGGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTATAGAGGTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTTGTTTACCCAC
 CCCACATCTCACACATCCAGAATTCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSSTTSLLSNYWFGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNSTQEYVQYNWETGDDRFSSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRS PGDGGPHDVFTSLPSDCQLGSRRLTTCLE
LWLGLLHGLALLHLLHGVGCHHLQHVHQDGAGVQVQA

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FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTGAGCTTTGGCCAGATGTTGGTTACCCCTTGCTCCTGT
TCTTTATGTCCTTTCTCCTCTTCTTATTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCCTGCCCTATTCTCCTCCCAA
GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
AGCCACCTCCCTGTCAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTAG
GACATTCGCCCTGTGTGCCACCAAACAGGACTTTCCTTGGCTTGGCATCCCTGGCTCT
CTCCTGGTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTTCAAGCTCCGTACT
ATGGCGATGGCCATGATGTTACAATCCCACTTGCTGAATAATCAAGTGGGAAGGGGAAGCA
GAGGGAAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACAAA
GGGAAGCAACAGGAACCTTCTGCAACTGGTTTTATCGGAAAGATCATCTGCCTGCAGATGC
TGTTGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
ATAGAACAGTCTGCTGGGAGTCAGACCTGGAATTCTGATCCAACTCTTTATTACTTTGGG
AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
AACCAAGGAAACTAACAATGTAGGTTACTAGTGAATACCCAATGGTTTCTCCAATTATGCC
CATGCCACCAAAACAATAAAACAAAATTCTCTAACACTGAAA

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FIGURE 192

MWLPLGLLSLCLSPPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCDLYDRATSPPLKCSLL

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MWLPLGLLSLCLSPPLPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQGSGME
HRNHLCFCDLYDRATSPPLKCSLL

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCTGGAGCCAGGAGGACGTCA
 CCGCG**A**TGGCAGGCATCAAAGCTTTGATTAGTTTGTCTCTTGGAGGAGCAATCGGACTGATGTTTTTGTAGTCTT
 GGATGTGCCCTTCCAATATACAAACAAATCTGGCCCTCTTTGGTCTATTTTTTACACTCTTCACTTATTC
 ATACTGCATAGCAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGTAAAGAACTTGCACCTCTTTC
 TTACAAAGGGCATTGTGCTGTACGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACATCTGATTGAGTGGGGA
 GCTTGTGCATCTGTTCTCACAGGAACACAGTCACTTTTGGAACTATACTAGGCTTTTCTGGTCTTTGGAAAG
 CAATGACGACTTCACTGGCAGCTGAGTGGTGA**AA**AAAGAAATACTGAACATTTGTCAATGGACTCTGCTCAATT
 GTTGGCCATTCAAGCACAGGAGATGGGCACTTAATGCTGAATGGTATAGCAAGCCCTCTTGGGGGTATTTTA
 GGTGCTCCCTCTCACTTTTATTGTAAGCATACTATTTTCAAGAGACTTGTGGAAGGATTAAGAGGATTTCT
 CTTTTGAAAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTTTGGGTGCTCGCTGAATTTAAATAT
 TTATGTGTTTTTCTGTTAGGTTGATTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAATGTAATCA
 TTTCATTGGTTAGGAATTCAGAATTCGCCGCGCTATTACTGGTCAAGTACATCTTTCTCTTAAATTTATT
 TAGCTCCATTATTACAAAAAATTATAAAAAAAGTTTTTCACTGAGTCAAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATAAGTTATAGACTGTATCTCAGTGCAAATATAGCTGCATTATACCTCAGAG
 GGGCCAAAGTGTAAATGCCCATGCCCTCCGTTAAGGGTTTGTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAAATTATTTATGGAATGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAGAAGAAATTTATGTTAAACTTTA
 AGSTAAGGGTGTAAAAACATTTTTGAGATAAGGTTTTTATTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGAGAAGATGACATTGAAATTCAGATTTTTGAATCCTGTTTCTATTTATAAGTGAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTACCCTGTAAATAGGACATACATGGAACCACTACTGATGAGGGACAGTTGTATGTTGC
 ATCATATATGCCAGAAAACTTCTCTGCTTCTCCTTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAAATATAGTTTAAATAACACTTAGAAGTGTTTACTTACCTGGAAAAAATTTGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGGCCCTTGCCATGATTAACAGTAACCTTGTAGTCTTACAGATTAATTCATGCA
 TTAACAGTTTAAGATTAGACCATGGTAATAGTAGTCTTATCTCTAAGGTTATATCATATGTAATTTAAAG
 TATTTTTAAGACAAGTTTCTGTATACCTCTGAACCTGTTTGTATTTGAGTTTATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCATTGTGTGTGAGTTAATGCAAGTAGCCAAGTCCAGCTATATAGCAGCTTACAGAAACAT
 ACCTGACCAAAAAATCCAGTAACCAAGGCATGATCAATTTATAGTGGTGTGTTACATCTAATAATTATCAGGA
 CTTTTTTCAGGAGTGGGTATAAAAAACATTCAAGTTGGTCTGACAGTATTTTGTAAAGGATATTTGTTGTATG
 TTTATTCAGTATACTTACATAAAAAATTATTCGCCATCAGCCAAACTCAGTAATCATGACAGCTGTCTGTTGT
 TTTATGAAGTTTATTTCTCAAGAAATGGGAATAAATTTGGGATTGTTCTAGCTTTTTTACTAAAGATGCCTAA
 AGCCACAGGTTTTATTGGCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG
 GCGTGTGGCTGGAGCCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTATATGTTTCAGATTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGCTGGTGAGACAGTTGGGAACCTTTTGTGCTTGTGATCTACTGGACTTT
 TTTTTTCAGGAAGATGCATTCTCTGCTCTCCCTATTTTCTGTTCTGGATGTCATGTCATGCATGCTACTG
 TTTTATCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTATTTCTATATACTAATTCGATTGGCAGCAT
 GTGCTCTTGACCTTGATATAGTCTGACATAGTGCTGCTCTGATTTCTAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGATATGACATGACATGATCAACATTACCTATTCTCTATGGAAGAAACCTTTTGTATGATGAACAATAA
 AGATTTTAAATATCTATTTTAAAAA

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FIGURE 194

MAGIKALISLSFGGAIGLMFLMGLCALPIYNKYWPLFVLFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW

[illegible]

FIGURE 197

GTGCAAGGAGCCGAGGCGAGATGGGCGTCCTGGGCCGGGTCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCAGGACCCCGTGCGCCGGCGGCCCGTTGAGTTCCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTCACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTTCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCTGCCCTGCCGC
CACGACGACGTCTTCTTTCCGCCTAGTGCCTCCTTCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGCGCTCCCGCGCGGGCGCCTACGCTTCCACGGGCCGGGCGCGCTGGACGGTG
GGCCCCGAGGACTGCGCGGACCCGTGGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCCT

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FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPLDGELVLASGAGFGVSDVGSHLDCGAGEPAVFRDSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRTFTTRDEDLAVFLASR
AGRLRFHGPALSVGPEDCADPSGCVCGNAEAQPWICAALLQP

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FIGURE 199

ATCGCATCAATTGGGAGTACCATCTTCCTCATGGGACCAGTGAAACAGCTGAAGCGAATGTT
TGAGCCCTACTCGTTTTGATTGCAACTATCATGGTGCTGTTGTGTTTTGCACCTACCCTGTGTT
CTGCCTTTTGGTGGCATAACAAGGGACTTGCACTTATCTTCTGCATTTTGCAGTCTTTGGCA
TTGACGTGGTACAGCCTTTTCCTTCATACCATTGCAAGGGATGCTGTGAAGAAGTGTGTTTGC
CGTGTGTCTTGCATAATTTCATGGCCAGTTTTATGAAGCTTTGGAAGGCACTATGGACAGAAG
CTGGTGGACAGTTTTGTAACATATCTTCGAAACCTCTGTCTTACAGACATGTGCCTTTTATCT
TGCAGCAATGTGTTGCTTGTGATTGCAACATTTGAGGGTACTTTTGAAGCAACAATACAT
TCTCGAACCTGAATGTCAGTAGCACAGGATGAGAAGTGGGTCTGTATCTTGTGGAGTGGAA
TCTTCCTCATGTACCTGTTTCTCTCTGGATGTTGTCCCACTGAATCCCATGAATACAAAC
CTATTCAGCAACAGCAA
AAAAAAAAAAAAAAAAAAAAA

1000
900
800
700
600
500
400
300
200
100
0
1000
900
800
700
600
500
400
300
200
100
0

FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGGTTCGGGGGCGTTCTCCAGTCAACCTCCCGCGGTACCCGCGGCGCGC
 CCGAGGGAGTCTCTCTCAGACCTCTCTCCCGTTCGCTCCAACTAATACGGACTGAACGGATCGCTGCGAGGGT
 GGGAGAGAAAATTAGGGGGAGAAAGGACAGAGAGAGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAATAGTCTCGAAATTTATCTGGTGTCTCTTCACTCTGCTGCACTGAGTCTTTC
 AACCACCTTTTCTCTCCAATAGACCCAGCAAAGGTTCTACTAGTTCTTCTTGGATGGATTCCGTTGGGATTACT
 TATATAAAGTCTCAACGCCCTATTTTCATTATATTTATGAATATGGTGTTCACGTGAAGCAAGTTACTAATGTT
 TTTATATCAAAAACCTACCTCTACCATTTACTTTGGTAACCTGGCTCTTTGCAGAGAATCATGGGATTGTTGC
 AATGATATGTTTGTATCTCTATTCGGAACAATCTTCTCTCTGGATCACATGAATATTTATGATTCCAAGTTTT
 GGGAGAAGCGACACCAATATGGATCACAACCAGAGGGCAGGCATACATAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAATACATAGCGCTTTCTTACTCATTACATGCCTTACAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAAATTTGTTGAATGTTTACGTCAAAGAGCCCATAAATCTTGGTCTTCTCTATTGGGAAGACCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCTTTTCAGATATTGACAAGAAGTTA
 GGTATCTCTATACAAATGCTGAAAAGGCAAAGTTTGGAAACACTCTGAACCTAATCATCACAAGTGATCATGG
 AATGACGCGAGTGCTCTGAGSAAAGGTTAATAGAATTTGACCAGTACCTGGATAAAGACCACTATACCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGGCAAAGAAGGTAATTTGATGAAGTCTATGAAGCACTAATCTACGCT
 CATCCTTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTACAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGGCTGATGAAGGGTGGCACATTTTACAGAATAAGTCAGATGACTTCTGTTAGGCAACC
 ACGGTTACGATAATGCGTTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAGAAATTT
 TCAAAAGAAGCCATGAATCCACAGATTTGTACCCACTACTATGCCACCTCTCAATATCACTGCCATGCCACA
 CAATGGATCATTCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGGTGGTCCCTTATACACAGAGTA
 CTATCTCTCTCCCTGGTAGTGTTAAACCCAGCAGAATATGACCAAGAGGGGTCATACCTCTATTTTCATAGGGGT
 TCTCTTGGCAGCATTATAGTGATTGTATTTTGTAAATTTTCATTAAAGCATTAAATTCACAGTCAAAATAGCTGC
 CTTACAAGATATGCATGCTGAATAGCTCAACCATTTATTAACGCCTAATGTTACTTTGAAGTGGATTGTCATA
 TTGAAGTGGAGATTCCATAAATATGTCAGTGTTTAAAGGTTTCAAATTTCTGGGAAACAGTTTCAAACATCTGC
 AGAAACCATTAAGCAGTTACATATTTAGGTATACACACACACACACACATACACACACAGGACCAAA
 ATACTTACACCTGCAAGGAATAAAGATGTAGAGTATGTCCTATTGTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGACTTTGGCGCAGATATGTATATTTTACCAACTTTGCACTATGTAAGTACCTTTATAT
 ATTGCACTTTAAATTTCTCTCTGATGGGTACTTTAATTTGAATGCACCTTTATGGACAGTATGCTCTTATATC
 TTGATTGAAATGACAACTTTTGCACCCATGTACAGAATACTTGTACGCATTGTTCAAACCTGAAGGAAAT
 TCTAATAATCCGGAATAATGAACATAGAAATCTATCTCCATAAATGAGAGAAGAAGAAGGTGATAAGCTTGA
 AAATTAATGTGATAACCTTTGAACCTTGAATTTTGAGATGTTATTTCCAAACAGCAGAATGCAACTGTGGGCAT
 TCTCTGTCTTATTTCTTCCAGAGAAGTGGTTTTCATTTATTTTCCCTCAAAAGAGAGTCAAACTACTGCAG
 ATTCGTGTAAATATATTTCTGTGCATAAATATTGTTGATTTCCTGATGAGTATATTAATCTGATTATTTCA
 TAATATGAGACACATGATATACCTTTCTCTATATAGTTACGAAATGGCTGAATAGAGACACAGGCA
 CCATCTCGCAATGTTTCTCTGTTGTAATTTTGTCTCTTGAATTAATTAATTAATTAATTAATTAATTAATTAAT
 AAATCAATTTGGATAAAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSSTFSLQLDQQKVLVSVFDGFRWDYLYKVPTPHFYIMKYGVHVK
 QVTNVFITKTPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRAGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTLLDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPLLCHLLNITAMPHNGSFWNVQDLLNSAMP RVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTGCTCCACGGGCGGGACCTTTGTAAGTGCAGGAGGCCAG
 GACAGGCCACCCCTGCGGGGCGGAGGCAGCCGGGTGAGGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCCTTGCCCTGGGTACACAGCCAAAGGAGGCAGAGCCAGAAGTACAA
 CCAGATCCAGAGGCAACAGGGAC**CATG**GCCACCTGGGACGAAAAGGCAGTCAACCCGAGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCTTAAGGCACCTTCACGGTCGTGGGAGACGA
 CTACCATGCCTGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCACTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCTGACGTTGCC
 CCTGCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTCTGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCCACTACATGAGCATCACCATCTTGGTCTTTTTTATGATGGAGATCATCTTTAAATT
 ATTTGTCTTCCGCCTGAGTCTTTTACCACAAAGTTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTTCATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGGTGGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGAC**TGAT**GAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTCAGATTACAAATCACACAGAGCATCTGCCTGTTTCAATCACAAAGAGAACAAACC
 AAAATCTATAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MATWDEKAVTRRAKVAPAERM SKFLRHFTVVGDDYHAWNIN YKKWENEEEEEEEQPPPTFV
SGEEGRAAPDVAPAPGPAPRAPLDFRGMRLKLFSSHRFQV I ICLVVDALLVLAEILIDL
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLLSSFTTSLRSMMPVVVVVSFILDI
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLLRLLQMQNVQLAAKIQHLEFS
CSEKPLD

FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCGAGTGGAGCACCCAGCAGGCCGCCAACAT
 GCTCTGCTGTGTGCTGTACGTGCCGGTTCATCGGGGAAGCCAGACCGAGTTCCAGTACTTTTG
 AGTCGAAGGGGCTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCATCCCTCC
 CAGGAATTTCCACCTACCGCCAGTGGAAAGCAGAAAATTTGTAAGCTGGAGATAAGGACCT
 TGATGGGCAGTACACTTTGAAGAATTTGTCCATTATCTCAAGATCATGACAGATAAGCTGA
 GGCTGGTGTTTAAGATTTTGGACAAAAAAGATGATGGACGCTATTGACGGCAGGAGATCATG
 CAGTCCGTCGGGACTTTGGGAGTCAAGATATCTGAACAGCAGGACGAGAAAAAATTTCAAGAG
 CATGGATAAAAAAGGCAGATGACCATCGACTGGAACGAGTGGAGAGACATACCACCTCTCTCC
 ACCCGTGGAAAAATCTCCCGAGATCATCTCTACTGGAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTACAGTGGAGGAGAGGCAGACGGGGATGTGTG
 GAGACACTGGTGGCAGGAGTGGGCGAGGGGCGGTATCCAGAACCTGCACGGCCCTCCCTGG
 ACAGGCTCAAGGTGCTCATGCAGGTCCATGCCCTCCCGCAGCAACAACTGGGCATCGTTGGT
 GGCTTCACTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGGCAATGGCATCAA
 CGTCTCTAAAATTTGCCCGGAATCAGCCATCAAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGGTAGTGACAGGAGACTCTGAGGATTCACGAGAGGCTTGTGGCAGGGTCTTTGGCA
 GGGGCCATCGCCAGAGCAGCATCTACCCCAATGGAGTCTTGAAGACCCGGATGGCGCTGCG
 GAAGACAGGCCAGTACTCAGGAATGCTGGACTGCGCCAGGAGATCTGGCCAGAGAGGGG
 TGGCGCGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCTATCCCGGCATC
 GACCTTGCAGTCTACGAGACGCTCAAGAATGCTGCTGACAGCAGTACTGAGTGAACAGCGC
 GGACCCCGGCGTGTGTTGTCTCTGGCCTGTGGCACCATGTCCAGTACTGTGGCCAGCTGG
 CCAGTCACTCCCTGGCCCTAGTCAGGACCCGGATCGAGGCGCAAGCCCTCTATTGAGGGCGCT
 CCGGAGGTGACCATGAGCAGCCTCTTCAAACATATCTCGCGACCGTGAAGGGGGCTCTGGGCT
 GTACGGGGGCTGGCCCAACTTCATGAAGTTCATCCCACTGTGAGCATCAGCTACGTTGG
 TCTACGAAACCTGAAGATCACCCTGGGCGTGCAGTCCGCGTGAAGGGGGGAGGGCGCGCCG
 CGAGTGGACTCGCTGATCTGGGCGCGAGCCTGGGCTGTGCAGCATCTCATTTCTGTAATG
 TGCCAAACATTAAGTGTCTCGAGGCCAAGCTGTGAAAACCTTAGACACCTCCCGCAGGAGGTT
 GGGGAGAGCTGGGAGCCTCCAGGGCTTGTCTGTGACCCAGCAGACCTCTGTTGTTTCC
 AGCGAAGACCAAGGCTATCTCTAGGGTCCAGGGTCAAGGCTCCGGGCTCACATGTGTAA
 GGAGAGACATTTTCTGCAGTGCCTGCCAATAGTGAGCTTGGAGCCTGGAGGCCGCTTAGT
 TCTTCCATTTTACCCTTGCAGCCAGCTGTGGCCACGGCCCTGCCCTCTGCTGTGCCGTGC
 ATCTCCCTGTGCCCTCTTGTGCCCTGCTGTGCTGAGGTAAGTGGGAGGAGGCTACAG
 CCCACATCCACCCCTCGTCCAATCCCATATCCATGATGAAAGGTTGAGGTCACGTTGGCCT
 CCCAGCTGCACTTCCCAACCTACAGCATTTGACGCCAACTTGGCTGTGAAGGAAGAGGAAG
 GATCTGGCCTTGTGGTCACTGGCATCTGAGCCCTGCTGATGGCTGGGGCTCTGGGGCATGCT
 TGGGAGTCAGGGGGCTCGGGCTGCTGGCCTGGCTGCACAGAAGGCCAAGTCTGGGGCTCA
 TGGTGCTCTGAGCTGGCCTGGACCTGTGAGGATGGGCCCCACCTCAGAACCAAACTCACTG
 TCCCCTGTGGCATGAGGGCAGTGGAGCACCATGTTTGAAGGGCGAAGGGCAGAGCCTTTGT
 GTGTTCTGGGGAGGGAAGGAAAAGTGTGGAGGGCTTAATTTATGAGTGTGTTGGGAAAAGGG
 TTTTGTCCAGAAGGACAAGCCGAGCAAAATGAGCGACTTCTGTGCTTCCAGAGGAAGCAGAGG
 GAGCAGGAGCTTGGCTGACTGCTCAGAGTCTGTCTGACGCCCTGGGGGTTCTGTCCAACC
 CCAGAGGGGCGCAGCGGAGCAGGCCCAACATTCACCTTGTGTGACTGCTTGAACCTATT
 ATTTTGTATTTATTTGAACAGAGTTATGTCTTAACATATTTTATAGATTGTTTAATTAATA
 GCTTGTGAATTTCAAGTTTATTTTATCATATTTATGTTATGTTGATTTGATCTGACCTTCCC
 AAGCCCGCCAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCGTGCAGTTCACAT
 CTGTCCAGAGAAATTCCTTTTGGGACTGGAGGCAGAAAGCGGCCAGAGGCGAGCCCTG
 GCTCCTTTCTTTGGCAGGTTGGGGAAGGGCTTGCCCCAGCCTTAGGATTTAGAGGTTTGA
 CTGGGGGCTGGAGAGAGAGGAGGAACCTCAATAACCTTGAAGTGGGAATCCAGTTATTTC
 CTGCGCTGCGAGGGTTTCTTTATTTCACTCTTTTCTGAATGTCAAGGCGAGTGGGTGCCCTCT
 CACTGTGAATTTGTGGTGGCGGGGCTGGAGGAGGGGTTGGGGGCTGGCTGCTGCCCTCC
 CAGCCTCTGCTGCCCTTGCTTAACAAATGCCGGCCAAGTGGCGACCTCACGGTGCACCTTCC
 ATTCACCAAGATGACCTGATGAGGAAATCTTCAATAGGATGCAAGATCAATGCAAAAAAT
 GTTATATATGAACATATACTGAGTCTGCTAAAAAGCAAAATTAAGAAAGAAATTTGACGTTAG
 AAGTTGTCAATTTAAAGCAGCCTCTCAATAAAGTTGTTTCAAGCTGAAAAAATAAAAAA
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FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFI PSQEFSTYRQWKQKIVQAGDKD
LDGQLDFEEFVHYLQDHEKKRLRVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
WRHLVAGGGAGAVSRCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGATAQSSIYPMEVLKTRMAL
RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNAWLQHYAVNS
ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSLFKHILRTEGAFG
LYRGLAPNFMKVI PAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGC**CA**
GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGGAG
 CAATTGCACTCATCATTGGCTTTGGTATTTACGGGAGACACTCCATCAGTCACACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACCTTTTGAACCTGACATCAA
 ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGC AAAAGATGAGCTGTCGGAGCAGGATGAAATGTTGAGAGCCGGACAGCAGTGT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGCTAACCTTGAGTATA
 AAACCTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCGATGGTTCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTACGATCAACAACACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAAGGCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTGTCTCTTCTTTTGGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCCCTGGCCACAAAAAG
 CATGCAAGTCAATTGTTACAACAGGGATCTACAGAACTATTTACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAAA
 GACATATTAGAAGTTGGGAAAATAATTCTATGTGAAGTGAAGTGTGTTAAGAGTGATAAG
 TAAATGACAGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTCACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCCTGAAAGTCTATCCCAACATATCCACATCTTATATTTCCA
 CAAATTAAGCTGTAGTATGTACCTAAGACGCTGCTAATTGACTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCT
 TGGCTTCTCTTCCCACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

FIGURE 208

MASLGQILFWSIISIIIIILAGAIALIIGFGISGRHSITVTTVASAGNIGEDGILSCTFEPDI
KLSDIVIQWLKEGVLGLVHEFKEGKDELSEQDEMFRGRTAVFADQVIVGNASLRLKNVQLTD
AGTYKCYIITSKGKGNANLEYKTGAFSMPEVNVVDYNASSETLRCEAPRWFPQPTVVWASQVD
QGAFSEVSNTSFEIENSVMTKVVSVLNVNTINNTYSCMIENDIAKATGDIKVTESIARR
SHLQLLSKASLCVSSFFFAISWALLPLSPYMLK

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FIGURE 209

GAATTTGTAGAAGACAGCGCGTTGCC**ATG**CGCGCTCTCTGGGCGAGTGTTGGCTCTGGT
 GCTGGTGGCGCTCTCTGGGGTGGCACGACGCCGTGCTGAAGCGGGCTCCGCCGGCCTGC
 AGCGGGTTCATGAGCCGACCTGGGCCAGCAGTTGCTACAGGAGATGAAGACCCTTCTTG
 AATACTGAGTACCTGATGCCCTTTCTCCTCAACCAGTGTGGATCCCTTCTCTATTACCTCAC
 CTTGGCATCGACAGATCTGACCCTGGCTGTGCCCATCTGTAACCTCTGCGCTATCATCTTCA
 CACTGATTGTTGGGAAGGCCCTTGGAGAAGATATTGGTGGAAAACGTAAGTTAGACTACTGC
 GAGTGGGGACGCGAGCTCTGTGGATCTCGACATACCTGTGTTAGTTCCTTCCCAGAACCCT
 CTCCCAGAGTGGGTGAGGACACGGCCTTTTCCCATCCTGCCCTTCTCTGCGAGCTGTTTT
 GCTTCCTTGTGGCCATCAGAGTTCCCTTCCCCTGGACAGCTGTGGAGAAAGACAGAGGCTGGG
 GTTTGGGAT**TGA**AGACCAGACCCCATCTGAGCCCTTCTCCAGCCCTGTACCAGCTCCTACT
 GGCATGGCTGAGCTCAGACCCTCCTGATTTCTGCCATTATATCCAGGAGCAGTTGCTGGCAT
 GGTGCTCACCGTGATAGGAATTTCACTCTGCATCACAAGCTCAGTGAGTAAGACCAGGGGC
 AACAGTCTACCCCTTTGAGTGGGCGAACCACCTTCCAGCTCTGTGCTCCAGGAAGCCCT
 GGGCATGAAGTGCTGGCAGTGAGCGGATGGACCTAGCACTTCCCCTCTCTGGCCTTAGCTT
 CCTCCTCTCTTATGGGGATAACAGCTACCTCATGGATCACAATAAGAGAACAGAGTGAAAG
 AGTTTTGTAACCTTCAAGTGCTGTTCAAGTGGCGGGGATTTAGCACAGGAGACTCTACGCTCA
 CCCTCAGCAACCTTTCTGCCCCAGCAGCTCTCTTCTGCTAACATCTCAGGCTCCCAGCCCA
 GCCACCATTACTGTGGCCTGATCTGGAATCATGGTGGCAGGTTCCATGGACTGCAGAAT
 CCAGCTGCATGGAAAGGGCCAGCTGCAGACTTTGAGCCAGAAATGCAAAACGGGAGGCCTCTG
 GGACTCAGTCAGAGCGCTTTGGCTGAATGAGGGGTGAACCGAGGGAAGAAGGTGCGTCGGA
 GTGGCAGATGCAGGAAATGAGCTGTCTATTAGCCTTGCCCTGCCCCACCCATGAGGTAGGCAG
 AAATCCTCACTGCCAGCCCTCTTAAACAGGTAGAGAGCTGTGAGCCCCAGCCCCACCTGAC
 TCCAGCACACCTGGCGAGTAGTAGCTGTCAATAAATCTATGTAACAGACAAAAAAAAAAAA
 AA

FIGURE 211

CTTCTGTAGGACAGTCAACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCCTGCCAGGCTGTGCGAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTAGTGAAACGGCCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAACTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCCTCCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATG
 AATCTAATGGAACCTCCTGTGTCGGGAAGCCCTGGAATGCTATGAAGAAGAACAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCAGTAACGCCACCTGTGAGTTCTGTCTGGTGAAAACAAGACTCTTGGAGGAGTCA
 TCTTTCGAAAGTTTGAGTGTGCAAAATGTAAACAGCTTAACCCCCACGCTGTGACCAACCACT
 TCCCACAACGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCAGCCTCCTTCTCTG
 GGGACTGCTGCCCTTGAGGTCCTGGGGCTGCACCTTGTCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MKGILVAGITAVLVAAVESLSCVQCSWEKSCVNSIASECPHANTSCISSASSSLETVPV
 LYQNMFCSAENCSEETHITAFTHVHSAEEHFHFVSQCCQGECSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGPWKCYEEEQCVFLVAELKNDIESKSLVLKGCNSVSNATCQFLSGENK
 TLGGVIFRKFECAVNSLTPTSPAPTTSHNVGSKASLYLLALASLLLRGLLP

FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGGAGCGAAGGTAGGAGGCA
 GGGCTTGCCCTACTGGCCACCTCCCAACCCCAAGAGCCAGCCCCATGGTCCCCGCCGCCG
 GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGGCGGCGGGGGCCCCAAGGCCTG
 ACCCAGACTCCGACCGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCCATGACCCGAG
 CTACCGGAGCACCGCCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
 ATGATGCCATGGCCGACGCCGACCGCTGGCTGGACCAGCGGCTGCCGAGCTCTTGCCGCC
 ACGGTGTCCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
 GGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCCA
 ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
 ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
 CCTGAGCCAGTGGTCCACACCTGGGTCTACCCCGAGCCGGTGGCCGTCACCCTCACCCACAG
 CCATGCCATCTCCTGAGGATCTGCGGCTGGTGTGATGCCCTGGGGCCCGTGGCACTGCCAC
 TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGGCGCCT
 TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGGAGCACAAGCCTTGCACTATCAACAATGTC
 CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
 GCCTCTCAGAGCACCACAGTACCAGGACCACCACTACCCCTTCCCCACCATCCACCTCAG
 AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTTGGAAACGGGTCA
 GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
 GACAGAAACCAGAGGTAATGGCCACTTCATCCACATGAGGAGATGTGAGTATCTCAACCTCT
 CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTTAGTACAGAAAAACAAAAC TGAAAA
 CACAA

FIGURE 214

MVPAAGALLWVLLLNLGPRAGAQGLTQTPTEMQRVSLRFGGPMTRSyrSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEALLAATVSTGFsRSSAINeedGSSEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVMPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQCPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNLSVFTMQPIDRNQR

FIGURE 215

CCCGGGTCGACCCACGCGTCCGGGGGAAAGGATGCGCGGCTGCGGGCGCGGTTGGTCTGCTAGCTGGGGCA
 GCGGCCTGGCAGCGGCTCCAGGGCGACCGTGAGCCGGTGTACCGGACTGCGTACTGCAAGTGGCAAGAGCA
 GAATGCTCTGGGGGCGCTCTGAATCACTTCGCGTCCCGCAGCCCAATCTACATGAGCTAGCAGGCTGAGGCT
 GTCGGGAGCAGCTGTAAATATGAGTGATGTGGGTACCGTGGGCTCTACCTCCAGGAAGGTACAAAGTGCCCT
 CAGTTCCATGGCAAGTGGCCCTTCTCCGGTTCCTGTTCTTTCAAGAGCGGGCATCGGCCGTGGCTCGTTTCT
 CAATGGCTGCGCCAGCTGGTGATGCTTCGCGGCTACCGCAGCTTCGTGCCAGCGCTCTCCCCATGTACACAC
 CTGTGTGGCTCTCGCCTCGCTTCCCTCAATGCATGGTTCTGGTCCACAGCTTCCACCAAGGGACATGAGCA
 CTCACAGAGAAATGGACTACTTCTGTGCTCCACTGTCACTCTACACTCAATCTACCTGTGCTCGCTCAGGAC
 CGTGGGGCTGCAGCACCCAGCTGTGGTCACTGCTTCGCGGCTCTCTGTGCTCATGCTGACCGTGACGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGTGGCCAACTGGCTATTGGGCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTCTGTGAACCAAGCGCGGCTGCCACAGTGGCGCAAGTGGTGGTGGTCTT
 GCTGCTGCAAGGGGCTGTCCCTGCTCGAGCTGCTTACTTCCACCGCTCTTCTGGGTCTGGATGCCATGCCA
 TCTGGGCACATCAGCACCATCCCTGTCCAGTCTCTTTTTTCAGCTTCTGGGAAGATGACAGCGCTGTACCTGTGT
 AAGGAATCAGAGGACAAGTTCAGCTGGACTGAAGACCTTGGAGCGAGTTCGCCCAAGTGGGGATCTGCCCCC
 GCGCTGCTGGGCTCCCTTCTCCCTCAACCTTGAGATGATTTTCTCTTTTCAACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTGGGCTCACCAGCCTTGGAGTCTGTTCTAGGG
 AAGGCCTCCAGCATCTGGGACTCGAGAGTGGGAGCCCTTACCTCTGGAGCTGAAGTGGGTGGAAGTGA
 GTGTGTCTTAGCTCTACCGGGAGGACAGCTGCTGTTTCTCCCAACAGCCTCTCCCCACATCCCAAGCTG
 CTTGGCTGGGTCTTGAAGCCCTCTGTCTACCTGGGAGACCAGGGACCAAGCGCTTAGGGATACAGGGGGTCCC
 CTTCTGTACACCCCCCACCCTCTCCAGGACACCACTAGTGGTGGTGGTCTGATGCTTGTCTTTGGGACGCCAA
 GGTTCACGGCGATTCTCCCATGGGATCTTGGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTCAGGGCCAGGGCTCCAGCAAGCCAGGGCA
 AGGATCCTGTGCTGCTGTGCTGTGAGAGCCTGCCACCGTGTGCGGAGTGTGGGCCAGGCTGAGTGCAATAGG
 TGACAGGGCGGTGAGCATGGGCTGGGTGTGTGTGAGCTCAGGCTAGGTGCGCAGTGTGGAGACGGGTGTTGT
 CGGGGAAGAGTGTGGCTCAAAGTGTGTGTGTGAGGGGGTGGGTGTGTAGCTGGGTTAGGGGAACGTGTG
 TCGCGTGTGCTGGTGGCATGTGAGATGAGTGACTGCCGTGGAATGTGCCAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTACCATCAATAACTCTTGTGGAGCGCAGCTCTGCCCAAGACGCCACCTGGGCGGACAGC
 CAGGAGCTCTCCATGGCCAGGCTGCTGTGTGATGTTCCCTGTCTGGTGCCCTTTGCCCGCTCTCTGCAAAC
 CTCACAGGTCCTCCACACACAGTGCCCTCAGAAGCAGCCCTCGGAGGAGAGGAAGAAATGGGGATGGC
 TGGGGCTCTCTCCATCTCTCTTTTCTCCTTGCCCTTCGATGGCTGGGCTTCCCTCCAAACCTCCATTCCTCT
 GCTGCCAGCCCTTTGCCATAGCCGATTTTGGGAGGAGGAAGGGCGATTTGAGGGAAGGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTCCCTTCCAGAGGGTCTTACTGTTCAGGGTGCCCGCAGGGCAGGCAGGGGCC
 ACATGATGCTGTGCCCTGGTAAAGGTGACCCCTGCCATTTACAGCAGCCCTGGCATGTTCTGCCCCACAGG
 AATAGATGAGGGAGCTCCAGAACTTTCATCCCAAGGCAGTCTCCGTGGTTGAACAGCATGGATTTTGT
 CTTCTGCCCTGACCCCTTGTCCCTCTTGGAGGAGGGGAGCTATGCTAGGACTCCAACTCAGGGATCGGGTG
 GCGTGGCTAGCTTCTTTTGAATCTGAAACTTTTAAAGTGGGAGGTGGCAAGGATGTGCTTAATAATCAA
 TTCCAAGCTCAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWLLAWCLWNQR
RLPHVRKCVVVVLLQLGLSLELLDFPPLFWVLDAAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

GGCGCGCTGGAATTGIGGGAGTTGTGTCTGCCACTCGGCTGCCGGAGGCCGAAGGTCCTGTA
CTATGGCTCCCCAGAGCCTGCCTTCATCTAGGATGGCTCCTCTGGGCATGCTGCTTGGGCTG
CTGATGGCCGCTGCTTACCTTCTGCCTCAGTCATCAGAACCTGAAGGAGTTTGCCCTGAC
CAACCCAGAGAAGAGCAGCACCAAGAAACGGAGAGAAAAGAAACCAAGCCGAGGAGGAGC
TGGATGCCGAAGTCTCTGGAGTGTTCCACCCAGCGCATGAGTGGCAGGCCCTTCAGCCAGGG
CAGGCTGTCCCTGCAGGATCCACGTACGGCTGAATCTTCAGACTGGGGAAGAGAGGCCAAA
ACTCCAATATGAGGACAAGTTCGAAATAATTTGAAAGGCCAAAGGCTGGATATCAACACCA
ACACCTACACATCTCAGGATCTCAAGAGTGCACCTGGCAAAATTCAGGAGGGGGCAGAGATG
GAGAGTTCAAAGGAAGACAAGGCAAGGCAGGCTGAGGTAAAGCGGCTCTTCCGCCCCATTGA
GGAAGTGAAGAAAGACTTTGATGAGCTGAATGTTGTGCTATTGAGACTGACATGCAGATCATGG
TACGGCTGATCAACAAGTTTCAATAGTTCCAGCTCCAGTTTGGAGAGAAGATTTGCTGCGCT
TTTGATCTTGAATATTATGTCCATCAGATGGACAATGCCGAGGACCTGCTTCTTCTTGCTGG
TCTTCAAGTGGTGATCATAGTGGGCTGAAACGACAGAGCCCTCGTGAAGGAGTATGCTGCGT
TTGTGCTGGGCGCTGCCTTTTCCAGCAACCCCAAGGTCCAGGTGAGGCCATCGAAGGGGGA
GCCCTGCAGAAGCTGCTGGTCATCTTGCCACGAGCAGCCGCTCACTGCAAGAAGAAGGT
CCTGTTTGCACTGTGCTCCCTGCTGCGCCACTTCCCCTATGCCAGCGGCAGTTCCTGAAGC
TCGGGGGGCTGCAGGTCTGAGGACCCTGGTGCAGGAGAAGGGCACGGAGGTGCTCGCCGTG
CGCGTGGTCACACTGCTCTACGACCTGCTCAGGAGAAGATGTTGCCGAGGAGGAGGCTGA
GCTGACCAGGAGATGTCCCAGAGAAGCTGCAGCAGTATGCCAGGTACACCTCCTGCCAG
GCCGTGTGGGAACAGGGCTGGTGCGAGATCACGGCCCACTCCTGGCGCTGCCCGAGCATGAT
GCCCGTGAGAAGGTGCTGCAGACACTGGGCGTCTCCTGACCACCTGCCGGGACCGCTACCG
TCAGGACCCCCAGCTCGGCAGGACACTGGCCAGCCTGCAGGCTGAGTACCAGGTGCTGGCCA
GCCTGGAGCTGCAGGATGGTGAGGACAGGGGCTACTTCCAGGAGCTGCTGGGCTCTGTCAAC
AGCTTGCTGAAGGAGCTGAGATGAGGCCCCACACCAGGACTGGACTGGGATGCCGCTAGTGA
GGCTGAGGGGTGCCAGCGTGGGTGGGCTTCTCAGGCAGGAGGACATCTTGGCAGTGCTGGCT
TGCCACTTAATGGAACCTGAAGGCCAAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAA
AAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCA
AAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCAAAAAAAGGCA

FIGURE 218

MAPQSLPSSRMAPLGMILLMAACFTFCLSHQNLKEFALTNPEKSSTKETERKETKAEDEL
 DAEVLEVFHPHTEWQALQPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAASFSSNPKVQVEAIEGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRTLVQEKGEVLAVRVVTLVTEKMFEEEEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

TTTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTCATTTGGGGTTTCGGTTCCCCCCTTCCC
CTTCCCGGGGTTCTGGGGTGACATTCGACCGCCGCCCTCTGGTGGGTTCGGTTGCCACCCCA
CGGGACATCCCAGCTGGCGCGCCCTCCATTTTGGCTGCTGGTGAAGCCCCACCCCC
TTCCACCTTGACACAGC**ATG**GGGGCTGCGGTGTTTTTTGGCTGCACTTTTCGTGCGCTTTCGGC
CCCGCCTTCGGCGCTTTTCTTGATCACTGTGGCTGGGAGCCCGCTTCGCGTTATCATCTCTGGT
CGAGGGGACATTTTTTTCGGCTGGCTTCCCTGCTCTGCGCTCTGTGCTCTGGTTCACTCTGGT
TCCATGTGACCGACCGCTCAGATGCGCCGGCTCCAGTAGCGGCTTCCTAGTTTAAAGTGTCTGGT
GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCCATCTACAAGCTGCTTAAAGAAGGCAGA
TGAAGGGTTAGCATCGCTGAGTGAGGACGGGAAGATCACCCATCTCCATCCGCGACATGGCCCT
ATGTTTCTGGTCTCTCTCTCCGATATCATAGTGGTGTCTTCTCTGTATCAATATTATTTGGCT
GATGCACTTTGGGCGAGGTGTGGTGGGATCATGAGAGTACACCTATTACTTCCTGACATTC
AGCCTTTCTGACAGACGCCATTATCTGCTCCATACCTTTTGGGAGTTGTGTTCTTTGATG
CCTGTGAGAGGACGGTATCTGGGCTTTGGGCGCTGGTGGTGGGAGTACCTATCGATCATCG
GGACTGCATTTCTGAACCTCTGGTATGAGCGACCGCTGCTGCCCATCTATGCAGTCACTGT
TTCCATGGGGCTCTGGGCGCTTACCATACAGCTTGAGGGTCCCTCCGAAGTATTTCAGCGCAGCC
TCTTGTGTAAAGGAC**TGA**CTACCTGGACTGATCGCCTGACAGATCCCACCTGCCCTGCTCCACTG
CCCATGACTGAGCCGACGCCACGCCGGGTTCATTGCCACATTTCTGTCTCTCTCTCTGT
GGTCTACCCCACTACCTCTCCAGGGTTTGTCTTGTGCTTTTGTGACCGTGTAGTCTCTAAGTGT
TACAGGACGAGCGCTGGGTTCAGCCAGTCACTGATGACTGGTGGGTTTGAATCTGCATCTATCCC
CACCACCTGGGGACCCCTTGTGTGTTCCAGGACTCCCCCTGTGTCACTGCTCTGCTCTCAC
CTTCGCCAAAGACTACCTCCCTCCCCCTCGAGCGCCAGCGAGGAGGAGCTCGGGTGAT
GGTGATTTCTGCCCTGCGCATCCCCACGAGGACTGAGGAACTAGAGGAGGACCCCTGGGC
CTGGGTTGCCCTCTGATGCTCGGCCGTATTCTTCATCTCCAGTTCTGGACAGTGACG
GTTGCCAAGAAAGGGACCTAGTTTATGCCATTGCCCTGGAGATGAATTAATGGAGGCTCAA
GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTCTC
AGGCTGAGGGGGAGAACATTTTGTGTGTGATAAATACCTAAACTGCCCTTTTTCTTTTTT
GAGTGGGGGGAGGAGGAGGTATATTGGAACTCTCTAACCTCTTGGGCTATATTTTCTC
TCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTCTCCTTGGTCCAGACCTT
GGGGGAAAGGAAGGAAGTGATGTTTGGGAAGCTGGCATCTGGAACATAATGGTTTAAACCT
CCTTAACACCAAGCATCTCTCTCTCCCAAGGTGAAGTGAGGGGTGCTGTGGTGAGCTGGC
CATCTCAGAGCTCGAGTGCCACTGGAGGATCAGACTAGCCATGACATCGTAGGGAAGGAGG
GAGATTTTTTTGTAGTTTTTAATTGGGGTGTGGAGGGCGGGAGGTTTTCTATAAAGTGT
ATCATTTTCTGCTGAGGGTGGAGTGTCCCATCTCTTTAATCAAGGTGATTGTGATTTTGAAT
ATAAAAAAAGAAATTTGTAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPFALEFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLSEdGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIGHDSPYYFLTSAFLTAAIILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCKD

FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGCTTGAGTGAGGACGGAAGATCAACCCA
TTTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
TCACCCCTATTANTTCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNTCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTTTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCTATTAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTGGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTTCATTTGGGGTTTCGGTTTCCCCCCTTTCCCTTTCCCG
GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
CCAGNTGGNGCGCCCTTCCCATTTGCCTGTCTGGTCAGGCCCCACCCCCCTTCCCACTG
ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACTTTCGTGCGTTTCGGCCCGGCCTTCG
CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGAGGGGCA
TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
CGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTGTGCC
TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
GCATCGCTGAGTGAGGACGGAAGATCACCCTCTCCATCCGCCAGATGGCCTATGTTTCTGG
TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTTG
GGCCAGGTGTGGTTGGGATCCATGGAGACTCACCC

FIGURE 224

GTAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCNCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCCTCCCATTTCCTGTCTGGTCAGGCCCCCACCCTTCCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACTTTCGTGCGGTTGGGCCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGCAGGGGC
ATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGTGCTGTCTCTGTC
CTTCTACAGGAGGTGTCCGCTTTCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTGGGATCCATGGAGAC

FIGURE 225

GCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCCAGAGCCAGGAGGAGCAG
 TGGCCAGGAAGGCACAGGCCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAGACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGTCTGTGCGTCCTGCACCCACATCTTTCTGTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATTCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCCGT
 CCTGTGGTTTCTCTCTACCTGGGGAAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTCACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACCACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCGGGGAAGACGCCCGGTGGGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCACGGCCGCCCACTGCAG
 GAAGAAAGTTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATCAAACCTGAACAGAAGAATTCGTCCCCTAAAGATGTGAGCCCAT
 CAACGTCTCCTCTCATTTGTCCCTCTGCTGGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCAAGTGCCTTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCCTGCCAGGGTGATTCTGGGGGCCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGCTCTGGGGAGATTACCCCTTGCGCCGGGCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGATCCAGGAAACCATCCAGGCCAACTCT**TGA**ATCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTCAG
 ACCCTCATTCCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGCTCTCTAGTTGAACCTGG
 GAACAATTTCCAAAACCTGTCCAGGGCGGGGTGGCTCTCAATCTCCCTGGGGCACTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAAAA

MATARPFPWMVLCALITALLGVTEHVLANNNDVSCDHPNSNTVPSSGNSQDLGAGAGEDARSDD
SSSRIRINGSDCDMHTQPWQAALLLRPNQLYCGAVLVHPQWLLTAHCRKKVFRVRLGHYSLS
FVYESGQQMFQGVKSIPHPGYSVPHGSNNDLMLIKLNRRIIPDMDVDRPINVSSHCPASGATKCL
VSGWGTTKSQVHFVKVQLCLNISVLSQKRCEDAIRPQIDTTFMCAGDKAGRDSQCGDSGGP
VVCNGSLQGLVSWGDPYPCARNRPNRGVYTNLCKFTKWIQETIQANS

MVNDRWKTMGGAAQLDRPRDKPQRPSCGYVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
APPPVSTGAASANSALVTVTERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
QPRLVGDQEQELLDTLADQLPRLLARASELQTECMGLRKGHGTLGQGLSALQSEQGRLIQLL
SESQGHMAHLVNSVSDILDALQRDRGLGRPNKADLQRAARGTRPRGCATGSRPRDCLDVL
LSGQQDDGVYSVFPTHYPAGFQVYCDMRTDGGGWTVFQRREDGSVNFRRGWDAYRDGFGRLT
GEHWLGLKRIHALTTQAAEYHLVDLEDENGTAYARYGSFGVGLFSVDPEEDGYPLTVADYS
GTAGDSLKHKSGMRFTTKDRDSDHSENNCAAFYRGAWWYRNCHTNSNLNGQYLRGAHASYADG
VWSSSTGWQOYSLKFSSEMKIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTGAACTAGCTCACAGTAGCCCGCGCGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAGATGAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAGCTTGCAGGAAGTCTGCAGCATGTGGC
 TGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAGACAGCAAAAGTTGGGAG
 GACTGTAATATTTCTGCGCTTAGTGAAAACCTTACCATGCTGAAGATAAACAAACAAGAAGA
 CCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGCGAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
 CTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTGTACTAGTACAAAATGGGTTCTCGTG
 TTTCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACA
 AGAAGTCTTATTACATGCCACCAACCAACCTCAGAAACCCATAATGTCACTGTGCCTTCTTG
 GCTTAGAGATAACTTTTAGTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCAT
 GTCTTCTTACACTTGGTGAATAAGAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATTTCTTTTGTTTGTTTCAGTTCACTAGTCCCTTCCCATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCACTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTCTCTGTGTCCATTAAAGACTCTGATAATTG
 TCTCCCCCTCATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCTTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCTTATTTCTTCCATTGACCCATATTTATACCTTTTCA
 GTACTGAAGATTTAATAATAATAATGTAATACTGTGAAAAA

FIGURE 230

MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPSSSTWRPVALTLLTLCVLVLL
IGLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRE
LYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAAS
QSYSEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPPSRDCVAILNGMIFSKD
CKELKRCVCERRAGMVKPESLHVPPETLGED

2000 年 9 月

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGACACAGGGNCTCTTTTCAACGTGGCGACCAGTGGCCCTGACCCGTG
CTGACTTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTNTTCAAGTCCAGAATAAAGCTTGCAGGAAGNTGCAGCAT
GTGGCTGAAAAACTCTGTCTGAGCTGTATAACAAGCTGGAGGAACCTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACACCATCTCC

FIGURE 232

GCCGAGCGCAAGAACCTGCGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CCGGGATTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCGCCCGCGGGG
 CCGAGCCCTCCGATCCGCGCCCTCCCGGTCCCGCCCCCTCGGAGACTCTCTGGCTGCT
 CTGGGGGTTTCGCGGGGCGGGGACCGCGGTCCGGGCGCCATGCGGGCATCGCTGCTGCTG
 TCGGTGCTGCGGCGCGCAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTCACCTGAGCCCT
 GCTCAGCGTCACTGGGTGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTTG
 AGCTGCCGCGCGCGCGGAACACCAACGCGCGCGCGCGGGCCAACTCGGTGAGCCCGGAGCG
 GAGCGCGAGAAGCCCGGGGCGCGCAAGGCGCGGGGAGAATTGGGAGCCGCGCTCTTGCC
 CTACCACCTGTCACAGCCCGCGCAGGCCCGCAAAAAGGCCGTGAGGACCCGCTACATACGA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCAGCTGCC
 ACCTGGGCGTGGCCGTGAACCGACAGCTGGGGCACCGGCTGGAGCGTGTGGTGTCTCGAC
 GGGCGCACGGGGCGCGCGGGGCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCAGGGCGACGACTTTGAC
 TGGTTCTTCTTGGTGGCTGACACCACTTACACCGAGCGCACGGCCCTGGCACGCCTAAGTGG
 CCACCTCAGCCTGGGCTCCGCGGCCACCTGTACTGGCGGGCCCCAGGACTTCATCGGGC
 GAGAGCCCCACCCCGGCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGTCGCGCATGCTG
 TGTCAACAACCTCGGCGCCCACTGGAGGGCTGCGCAACGACATCGTCACTGCGCGCCCTGA
 CGATGGCTGGTGGTGGCTGATCTTCGATGCCACCGGGGTGGGTGCTGCTGTCAGCCAGG
 GGGTGCACTATAGCCATCTGGAGCTGAGCCCTGGGAGCCAGTGCAGGAGGGGGACCTCAT
 TTCCGAAGTGGCTGACAGCCACCTTGTGCGTGACCTGTGACATGTACCAGCTGCACAA
 AGCTTTTCGCCCGAGCTGAAGCTGGAAACGACAGTACAGGAGATCCAGGATGTACAGTGGGAGA
 TCCAGAATACCAAGCCATCTGGCCGTGATGAGGAGCCGGGCGAGCTTGGCCCGTGGGTATT
 CCAGCACCATCCCGCCCGGCGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTACCGGAGCA
 GCACGCTTTCTCTGCGCGCATGGCTCACCCCGCTGCCCACTGCGTGGGGTGACCGGGCTG
 ATGTGGCCGATGTTCTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTACCAACCGGGCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGGTATGGA
 ATACAGCTGGAATGCACTGGAGGCACTGACCCCCAGGAGGCGCGCGGCCCTCACTC
 CCGAGTGCAGCTGCTCCGGCCGCTGAGCGCGCTGGAGATCTTCCGCTGTGCCCTATGTCACT
 GAGGCTCACGCTCACTGTGCTGCTGCTCTAGCTGCGGCTGAGCGTGACCTGGCCCTTGG
 CTTCTTGGAGGCTTTGCCACTGCGAGCACTGAGCGCTGGTGTGCTGCGGCGAGCCCTGACC
 TGCTGCTACTGTATGAGCGCGGCCAGGCCAGCGCTGGCCATGCAAGATGTCTTCGACCT
 GTCAGGCGCCACGTGGCAGAGCTGGAGCGGCGTTTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGACAGACGCCGACCTTACCACCTGCGCCTCATGGATCTACTCTCCAAGAAGCACCCG
 TGGACACACTGTCTGCTGGCGGGGCCAGACAGCTGCTCAGCCTGACTTCTCTGAACCCG
 TGCGCATGTATGCCATCTCCGCTGGCAGGCTTCTTTCCATGCAATTTCCAAGCTCTCCA
 CCCAGGTGTGGCCCCACCAAGGGCTTGGGCCCCAGAGCTGGGCGTGACACTGGCCGCT
 TTGATCGCCAGGCGAGCGAGGCCCTGCTTACAACCTCCGACTGCTGGCAGCCCTGTGGG
 CGCTGGCGGCGAGCTCAGAACAGAAGAGGAGCTGCTGGAGGCCCTGGATGTGTACGAGCT
 GTTCTCCCACTTCTCCAGTCTGATGTGCTGCGGGCGGTGGAGCGCGCGCTGCTGACAGCT
 ACCGGGCGAGAGCTGACGCGGAGGCTCAGTGAGGAGCTGTACCAACCGCTGCTCCAGAGG
 GTGCTTGGGGCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGCAGGG
 CAACAGCACCTGAACCCCTGTCCCGCTGGGCGGTGGCATGGCCACACCCACCCACTT
 CTCCCCCAAACCAAGAGCCACTGCCAGCCTCGCTGGGAGGCTGGCCGTAGCCAGACCCCC
 AAGTGGCCCCCTGGTCCCTCTGCTGCTGCTGGGTCCCTGGGCTTGGACAGCACTGGG
 GGAGCTGCCCGCAGAGCCACCCACTTCTATCCAAACCAAGTTCCTGCGCCCCCTGAGCT
 GCTGATTCGGGCTGTGGCCTCCACGTATTATGCACTGACCTGCTGAGCCAGCCAGCTGCT
 CTCGCGGCTGGGGCTGGGCTGTAGAAGAGTGTGTGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCCACTTCTCCCTTTTGGACCTGCCGAAGCTCCCTGCGCTTAATAAACTGGCCA
 AGTGTGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWVEEPCGPGPPQPGDSELPPRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVTRYISTELGIRQRLLVAVL
TSQTTLPTLGAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFDWFLLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCILDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAELETTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDFTEQHAFCADGSPRCPLRGADRADVADVLTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPQGGRRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLRMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFPMHFQAFHPGVAPPQPGPPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLES LDVYELFLHFSSLHVLRAVEPALLQRYRAQTCSARLSEDL
YHRCQSVLEGLGSRTQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCTAGTGAGAGAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTTAGAAAGCTTGATTTCCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTCTTCCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCTCATTGGAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCT
 TTCCCCGCCCTGAGACCTGCAAGCACCATCTGTCT**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCCGTCTTTTGGCGGCGCGGCGACGCGAGGGCTCCCGGCCGCCGCTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCGCTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAAACCTTGATGAGAAGAACCA
 GACTCCCATGGTTATGACAAGGACCCCGTTTTGGACGCTTGGAACATGCGACTTGTCTCTT
 CTTTGGCGTCTCCATCATCCTGGTCCTTGGCAGCACCTTTGTGGCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAGGGGCTGAAAGTCTGAA

FIGURE 236

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGTCTTTTGGCGGCAGCGGCGACGCGAGGGC
TCCCGGCCGCCCGCGTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGGCGGGAAGCGGCCCCAGAACCAGCACACCGTGGCAAGAGGACCCAGAACCCGAGGA
CGAAAATTGTATGAGAAGAACCAGACTCCCATGGTTATGACAAGGACCCCGTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTGGCGTCTCCATCATCCTGGTCCTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATACCGAGAGGCCAATGGCCTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCTATGCGCGTGTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGCGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACCTGTGCATCACCCCGCTGCCTTCCGGGG
 ACGTAGCCGCGCCACATTCCAGTTCGCGACGCGCTGGGATTCGGAGCTTCAGCGGGGAAGGAGTG
 TCCCATTTACAGGCTCTTTCCCAAAGCCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCTATTACACAAGGCTTTTGGAGGACCCGATACTGGGGGCCACCCCTCTCTGC
 AGGCCCCATCAGGTGCAGAGCTGTGGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAAGGAGCTCAGTAATGTCTCTCAGGGATCTTCTGCGCTCTCTCAACTTCATCGA
 CTCCACCAACACAGTCACTCCCACTGCCTCTTCAAACCCCTGGGTCTGGCCAAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCGCGGGAGGTGGTGTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAGCTACCCTCCAGGCAGTGCATATCCGCCCTGTTGCAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCAAGTTGATTGTGCTTC
 ATCAGCGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCCGAACCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACCCCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCCGACCACTACATATCAGGACGTCTCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGGAAGAGACCCCCAGAGAATGAGGCCCCCCCAGTGCCCTTCTGTC
 ATGCCACGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACACTGCTGTAC
 AACCCCAACCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCTGGTATCTGCG
 GCTGTATGTGCACACCTCACCATCACTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGTGGCG
 GCCAACTAGTCAACAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCTAAACCATGGCTTCTATGTACGCCATCTGTCTCAGCGCCCTTGTGCCCCA
 GCATGGTAGCAGCCAGCCAGTGGACTGGGAAGAGAGTCCCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCCTACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGCACAGGT
 GGCTGGCCAAGCGCTGGCCAACCTTATCCGGCGCGCCGAGGTGTCCCCCACTCTGATT
 CTTGCCCTTTCCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGTCTCTCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACAGCTCAGGCG
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTGTAATTGTAATTAA
 CTTAGAATTATTCTTCTCACCTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTCGGTGGCTGCTGTATTGGACAGCACAGAAAAAGATTTCCATCACCACAGAAAAAGGT
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTGTGGAATAAAAAACGGCTGTTTCCGTGGAAAAA

MPLALLVLLLLPGGWCLAEPPRDSLREELVITPLPSGDVAATFQFTRWDSSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELVWVFQDVTVDVDSWK
ELSNVLSGIFCASLNFDISTNTVTPTASFKPLGLANDTDHYFLRYAVLPREVVCTENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRVCRNARCTSIISWELRQTLSSVVFDAFITG
QGKKDWSLFRMFRTLTPECPPLASESRVYVDITTYNQDNETLEVHPPTTTYQDVILGTRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLLDTVPWYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLEMLIQLPANS
VTSYIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLPFVSD
GKNVFRVRLYTEPLLVNLTPTPDFSMYPNVICLTCTVAVACYGSFYNLLTRTFHIEEPRTGGLA
KRLANLIRARGVPL

FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACTGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATGATGCTGGGTCTTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCCTGAGGGTCCTGAGACTTGAATATGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCCTTTTCCCCAAAAGAGGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCTCTCTACCTGGTGCTCCTCCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAAGTGCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCAGTGTGAGAGAAGAGAAAGTGGTCTCACCAGATG
CTGAATCTGCTGGTGCTTGATCTTGGAATCCCAGCCTCTAGAAGTGAAGAAATAAATAT
TTGCTGTTTATAATCAA

FIGURE 240

MGSSSFVLVMVSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEKGKDEDDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63

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FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATGTGTTAAGACAAAGGGTGTGCACTTCTCGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCAGAACCTTCC
 TCTAGAACCCGACCCACCACCATGAGGTCTCTGCCTGTGGAGATGCAGGCACCTGAGCCAAAGG
 CGTCCAGTGGTCTTGTCTTGGCTGTCTTGGTCTTCTTTCTCTTCGCCCTTGCCCTCTTTTA
 TTAAGGAGCCTCAAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCAGGCACCCACAAGGGCGAGGAGGACAACCATCTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCCAACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGGCCAGAAAAAGAGAAACCATGTGTGAACACACTGTC
 ACCCAGAGGGCAAGATGCAGGGATGGCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAGGAAATGGGGGCCAGACCAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAGAGAAGCACACAGGGCAAAGCGGCAACCCACAGCCAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCACCTAAGGAGAAGAACTCAGGCCACCCCAACCCCTGCCCTTTCCAG
 AGCCCCAGCAGCAGAGAACAAGACTGAAGGCCCACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCCTTCAGACGACTGCCCTGACCTGTG
 TGAAGATCAAGGCCTCAAAGTGCCTGTGGCTCCAGAACTCTTCTGCCCAACCTCACTCTC
 TTCTGGACTCCAGACACTTCAACCAGAGTGTAGTGGGACCCTGGAACACTTTGCACCACC
 CTTTGGCTTCATGGAGCTCAACTACTCCTTGGTGCAGAAGGTGCTGACACGCTTCCCTCCAG
 TGCCCCCAGCAGCAGTGCCTCTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGACATCACTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACCTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCCTTCTCCTGACCCAGTCACTCTTATATTGGGCAAT
 CGGGGTTTCAAGAACGTGCCTCTTGGGAAGGACGTCCGCTACTTGCACCTTCTGGAAGGCAC
 CCGGGACTATGAGTGGCTGGAAGCACTGCTTATGAATCAGACGGTGATGTCAAAAAACCTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCGGGAAGCCCTGCACATGGACAGGTACTGT
 TTGCTGCACCCAGACTTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCTTGGG
 TGGTGCCCACTGGAGGATATACCGCCCCACCACTGGGGCCCTCCTGCTGCTCACTGCCCTTC
 AGCTCTGTGACCAGGTGAGTGCTTATGGCTTCATCACTGAGGGCCATGAGCGCTTTCTGTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAGCGTCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAACTGAACGGGGCCAGGGCTGCCATGGTCTCCTTGCCCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGGAACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTCTTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAAATACCACAATTCCCTGTGAAAAACACTCTT
 CCACTGCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTTACAGAAACATATAGATCTGT
 GTTTGAATTCAGATCGAGTTTACAGTTGTGAATCTTGAAGTATTACTTACTTACTACTAC
 AGATTGTCTAGAAGACCTTTCTAGGAGTTATCTGATTCTAGAAGGGTCTATACCTTGTCTCTTG
 TCTTTAAGCTATTTGACAACTCTACGTGTGTAGAAAACGATATAATAACAAATGATTGTT
 GTCCATGGAAAGGCCAAATAAATTTCTACAGTGAAAAAAGAAAAA

FIGURE 242

MRSCLWRCRHLSQGVQWSLLLAFLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQGNNGQTRKLTASRTVSEKHQG
 KAATTAKTLIPKSQHRMLAPTGA VSTRTRQKGVTTAVIPPEKKPQATPPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLHFAFPFPGFMELNYSLVQKVVTFRFPVPQQQLLLASLPAGSLRCITCAVVGNGG
 ILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFAREALHMDRYLLHPDFL
 RYMKNRFLRSKTLGDAHWRIRPTTGALLLLTALQLCDQVSAYGFITEGHERFSDHYIDTSW
 KRLIFYINHDFKLEREVWKRLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCCTCCTCCTGGGGCTGCTGCTGGTGCTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAAACACT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAAACACTTCCATAGACTTTATCACACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAACCAACAGGGAAACAGAACTATCTTTATACACATCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTCCATAAGTCCTTTGAGTTTGTATGTTGTTG
ACAGTTTGCAGATATATATTCGATAAATCAGTGACTTGACAGTGTTATCTGTCACTTATTT

FIGURE 245

GGGCTGGGCCCCGCCGAGCTCCAGCTGGCCGGCTTGGTCTGCGGTCCCTTCTCTGGGAGG
CCCCACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGGCTCCGCCGGGCGCGCCG
CTCACCGCAATCGCTCTGTTGGTGTGGGGGCTCCCTTGGTGTGGCCGGCGAGGACTGCCT
GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTACCTTCT
GCTGCGGGACCTGTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
CCTCTTTGTGTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTCTGTGTACCTGT
ACCGCCGGCGCCAGCAGCTCCAGAGCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
TGGCTTCATGTACCCACCTAGTGGTCCCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
CAGTCTACAACCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
CCTGTACCTGCATCTGGTCTCGGGGTGGCAGGAGTCCCTCAGCCACCAGGCCCCAGACCAA
GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACTAGA
ACTATGAGGGGTTGGGGGGAGGGCTTGAATTATGGGCTATTTTACTGGGGGCAAGGGAGG
GAGATGACAGCCTGGGTCACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
CCAGGAAGCTGGGGCCCTACTGTTTGTCCCCTCTGGGCTGGGGTGGGGGAGGGAGAGGT
TCCGTGACGAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCACTGGCCACATCTCTGGCCTG
CTAGATTAAAGCTGTAAAGACAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
CRDLTLTLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICCFLCSCCYLYRRRQQLQSP
FEGQEIPMTGIPVQPVYPYPQDPKAGPAPPQPGFMYPSPGAPQYPLYPAGFPVYNPAAPPP
YMPQPQPSYPGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93

FIGURE 247

GGGGGAGCTAGGCCGGCGGCAGTGGTGGTGGCGGCGGCCGAAGGGTGAGGGCGGCCCCAGAA
 CCCACGGTAGGTAGAGCAAGAAGCATGGTGTCTTCTGCCCTCCAAATGGTCCCTTGAACCATG
 TCATTTCTACTTTCCCTACGTGTTGGCTCTCTTAAGTGTCCACTGCTTCCATGGTGTGTCAGAG
 CACTGAAGCATCTCCAAAACGTAGTGATGGGACACCAATTTCCCTTGGAAATAAAATACGACTTC
 CTGAGTACGTATCCCGAGTTCATTATGATCTCTTGATCCATGCAAAACCTTACCACGCTGACC
 TTCTGGGGAACCCAGAAAGTAGAAATACAGCCAGTCAGCCCACAGCCACCATCTCCCTGCA
 TAGTCACACCTGCGAGATATCTAGGGCCACCTTGTCATTCACTATGCTGGCAATCTTTCCGGAGAC
 AAGAACCCTGCGAGTCCCTGGAAACCCCCCTCAGGAGCAAAATGCACTGCTGGCTCCCGAG
 CCCCTCCTGTGCGGGCTCCCGTACACAGTTGTCATTCACTATGCTGGCAATCTTTCCGGAGAC
 TTTCCACGGATTTTACAAAAGCACTACAGAACCAAGGAAGGGGAACCTGAGGATACCTAGCAT
 CAACACAATTTGAACCCACTGCACTAGAATGGCCTTTCCCTGCTTTGATGAACCTGCCCTTC
 AAAGCAAGTTTCTCAATCAAAATAGAAAGAGAGCCAAAGCACCTAGCCATCTCCAATATGCC
 ATTGGTGAATCTGTGACTGTTGCTGAAGGACTCATAGAAGACCAATTTGATGTCACTGTGA
 AGATGAGCACCTATCTGGTGGCCTTCATCATTTAGATTTTGTGCTGTGACAGAAATAAC
 AAGAGTGGAGTCAAGGTTTCTGTTATGCTGTGCCAGACAAGATAAATCAAGCAGATTATGC
 ACTGGATGCTGCGGTGACTCTCTAGAAATTTATGAGGATATTTTCAAGCATACCGTATCCCC
 TACCCAAACAAGATCTTGCTGCTATTCCGCACTTTTCAGTCTGGTGTATGGAAACCTGGGGA
 CTGACAACATATAGAGAATCTGCTCTGTGTTGATGCAAGAAAGCTTCTGCACTCAAGTAA
 GCTTGGCATCAAGTCACTGTGGCCCATGAACCTGGCCACCACTGGTGGTGGGAACCTGGTCA
 CTATGGAATGGTGGAAATGATCTTTGGCTAAATGAAGGATTTGCCAAATTTATGAGGTTTGTG
 TCTGTCAGTGTGACCCATCTGAACCTGAAAGTTGGAGATTATTTCTTTGGCAAAATGTTTTGA
 CGCAATGGAGGTAGATGCTTTAAATTCCTCACACCTGTGTCTACACCTGTGGAAATCTGTG
 CTCAGATCCGGGAGATGTTTGTATGATGTTTCTTATGATAAGGGAGCTGTATTTCTGAATATG
 CTAAGGGAGTATCTTAGCGCTGACGCATTTAAAGTGGTATTGTACAGTATCTCCAGAAAGCA
 TGGCATCAGGAAGGGGTGGATGTGAAAACCATGATGAACACTTGGACACTGCAGAGGGGTTT
 TCCCTTAATAAACCATCACAGTGAGGGGGAGGAATGTACACATGAAGCAAGAGCATACATGA
 AGGGCTGTGACGGCGCCCGGCACACTGGGTACCTGTGGCATGTTCCATTGACATTCATCAC
 AGCAAAATCCAAGATGGTCCATCGATTTTGTCTAAAAACAAAAACAGATGTGCTCATCTCCCT
 AGAAGAGGTGGAATGGATCAAAATTTAATGTGGGCATGAATGGCTATTACATTGTGCATTAAG
 AGGATGATGGATGGGACTCTTTGACTGGCCTTTTAAAGGAACACACACAGCAGTCAGCAGT
 AATGATCGGGCAAGTCTCATTAACAATGCATTTCAAGCTCGTCAGCATTTGGGAAGCTGTCCAT
 TGAAAAGGCCTTGGATTTATCCCTGTACTTGAACATGAACCTGAAATTTATGCCCGTGTGTTT
 AAGGTTTGAATGAGCTGATTCCTATGTATAAGTTAATGGAGAAAAGAGATATGAATGAAGT
 GAAACTCAATCAAGGCCTTCTCATCAGGCTGCTAAGGGACCTCATTGATAAGCAGACATG
 GACAGACGAGGGCTCAGTCTCAGAGCAAAATGCTGCGGAGTGAACACTACTCCTCGCCTGTG
 TGCACAACATCAGCCGTGCGTACAGAGGGCAGAGGCTATTTCCAGAAAGTGGGAAGGAATCC
 AATGGAAACTTGAGCCTGCCCTGCTGCGACGTGACCTTGGCAGTGTGCTGTGGGGGCCAGAG
 CACAGAAGGCTGGGATTTTCTTATAGTAAATACAGTTTCTTGTTCAGTACTGAGAAAAG
 GCCAAATTTGAATTTTGGCTCTGCAAGAACCCAAAATAAGAAAAGCTTCAATGGCTACTAGAT
 GAAAGCTTTAAGGGAGATAAAATAAAAACTCAGGAGTTTCCACAAATTTCTTACACTCATTTG
 CAGGAACCCAGTAGGATACCCACTGGCCCTGGCAATTTCTGAGGAAAACCTGGAACAAACTTG
 TACAAAAGTTTGAATTTGGCTCATCTTCCATAGCCACATGGTAAATGGGTACAACAAATCAA
 TTCTCCACAAGAACACGGCTGAAGAGGTAAAAGGATTTCTCAGCTCTTTGAAAGAAAATGG
 TTCTCAGCTCGGTGTGTGCCAACAGACAATGAAACCATTTGAAGAAAACATCGGTTGGATGG
 ATAAGAAATTTGATAAAAATCAGAGTGTGGCTGCAAAAGTGAAGGATTTGACCTATGTGTA
 TTCTCCCTTGCCCGGTTCTGTTATCTCTAATCACCACATTTTGTGAGTGTATTTTCAA
 ACTAGAGATGGCTGTTTGGCTCCAACCTGGAGATATCTTTTCCCTCACTCATTTTGTGA
 CTATCCCTGTGAAAAGAATAGCTGTTAGTGTTTTTCATGAATGGGCTTTTTCATGAATGGGCT
 TCGCTACCATGTGTTTGTCTATCACAGGTGTGGCTGCAACCTGAAACCAAGTGTGGTGTG
 TCCCTGCCACAGAAGATAAAGTACCTTATTGTTCTCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTLTFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPQLQVLE
 HPPQEQIALLAPEPLLVGLFPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMEFVSVSVTHPELKVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNWTWLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVRHFLFKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPVFQGLNELIP
 MYKLMKRDMMNEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSLPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSTEKSQIEFALC
 RTQNKELQWLLDESFKGDKIKTQEFPPQILTLIGNPVGYPPLAWQFLRKNWNKLQKFELGS
 SSIAHVMVGGTTNQFSTRTRLEEVKGFSSSLKENGSQLRCVQQTETETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metalloproteinases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTCATGAGCGCGGTATTACTGCTGGCCCTCCTGGGGTTCATCCTCCAC
 TGCCAGGAGTGAGGCGCTGCTCTGCCAGTTTGGGACAGTTCAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGGCAATGGACCCCTAAGAACACCAGCTGCCACAGCGGCTTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGTCTCCAAGGGGTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCAAGGGGACCACACTGTTATGAT
 GGCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTATCGGGGGACCACCATTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATTGGACCACATCGAATACCGAGATGTGCGAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCTTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTTCCAGAAGACCACCATTCCACTCAGCCCCCTCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACCTCCCTCCCTCCTCAAGCTGCCCTGTCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGAACCTGTTCAAGTGGCTCCCCCGAATGACCTGCCCGAGG
 GGCGCCACTCATTGTTATGATGGGTACATTTCATCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTTCAGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTAACACACCAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGAGTGGTTTGCCCTTCTGCTAACTCTATTACCCCCACGATTCTTACCCTGCTGTA
 CCACCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGAGACACAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCACACACAATCATTCATATCTACTACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGAAGTGCCTATGGGAGAGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCCTGTCCTTTCA

MSAVLLLLALLGFILPLPGVQALLCQFGTVQHVKVSDLPRQWTPKNTSCDSGLGCQDTLMLI
ESGPQVSLVLSKGCTEAKDQEFRVTEHRMGFGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
PADPGSLRCPVCLSMEGCLEGTTEECPKGTHCYDGLRLRGGGIFSNLNRVQCGMPQPQGCN
LLNGTQEIGPVMGTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSTNTEMCVEVQVCQETL
LLIDVGLTSTLVGTGKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDLNCSASSSSVLLN
SLPPQAAPVPGDRQCPTCVPLGTCSGSPRMTCPRGATHCYDGYIHLSGGGLSTKMSIQGC
VAPQSSFLLNHTRQIGIFSAREKRDVPPASQHEGGGAEGLESLTWGVGLALAPALWGWVVC
PSC

FIGURE 251

GCGACGGGCAGGACGCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGGATGAGGGGGAATCTGGCCCTGGTGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGCGCCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTGTCAT
 GGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTCTGCCAGGGCCGCGGGGGCAGCTGAGCATGCCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCGTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCCAACATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGCTGGAACGACGTGGCCTGCCACACCACCATGTACTTCATGTGTGAGTTTGACAAG
 GAGAACATGTGAGCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCTGGGGTGTCTGTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCATTATGTAATTATTACCCAGAATTGCTCTTCATAAAGCTTGTGCCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCCTCTTTGCAGGAGCACC GG CAG
CACCAGTGTGTGAGGGAGCAGGCAGCGGTCTCTAGCCAGTTCCTTGATCCTGCCAGACCACC
CAGCCCCGGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTACAGCCAT
CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGG
TTCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
GGAGCGTCCAGCCAGAGGGAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCC
CTTCATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCTGGGAACAGAGGAGCAGAGACC
TTTTAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTGGCATCCTCAAGT
ATCCCCGAGAGCAGAATAGGTACTCCACTTCGGACTCCTGGACTGCATTAGGAAGACCTC
TTTCCTGTCCCAATCCCCAGGTGCGCACGCTCCTGTTACCTTTCTCTTCCCTGTTCTGT
AACATTCTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAAACTGCA
TAGTGAATATCCCCAACCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCTGTAGTGT
CCTACATTA AAAATATAATGTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRMDHDFVGLMGKRSPVQPEGKTPFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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GGGCGCTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
CGCGCTGTGCGCGCTGCTACCGCGTCTGCTGGACGCGGGAGACGCCAGCGAGCTGGTGATTG
GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCCAGGAGCCAGGCTGCCCGTGAGTC
CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCTCTGGTGGTGTGCATCCCCCTTGGGGC
TGCTGTTCTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGTCACTCTCTTAGAGGAG
CTGCTCAGCAAATACCAGCACACGAGTCTCACTCCCGGGTCTCGCAGAGCCATCCCCAGGGA
GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
CCAACATGGAGTACATGGTGAGCGCCGGCTCCCGCCCGCAGAGGCTGGCACCGGGGGTGGGGC
CTGGGCCACCAGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCCTGTGATGG
CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTGTGTTTGTGTT
TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGACAATCGTCAGCCCTG
AAACCTTAGACTCTCCGGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAATACAG
GCATGACCCATGTTGCCAGCTAGATTTTAAATATTTTGTGAGATGGGGTCTTGCTACGT
TGCCCAGGCTGGTCTTGAACCTCTTAGGCTCAAGCAATATCTCCTGCTTCAGCCTCTCAAAGTG
CTAGGATTATAGGCATGAGTACCCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
ACAACACACGTGGGTTCCCTGTGCAGAGCCTGCCTCGTTGCCTTCATGTCACTCTTGGTAGC
TCCACTGGGAACACAGCTCTCAGCCTTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCCTGACTTCTC
CTTAGCCCGTGTGAGCCTCACTTTCACTTTGGAGAGTCTTCTCTCGCTGGTTGCCATGACT
GTGAGATAAGTCGAGGCTGTGAAGGGCCCCGCGACAGACTGACCTGCCTCCCCAACCCCTAGG
CTTTGCTAAACGGGAAAGGAGCTTAACGGTGACAGAAAGACAGCCAAGGTCAACCCCTCCCGGT
GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
TGGAAGCTTCCTTCTGGCTGGTTTTCCAGAAGCTACAGAGGAATGGACCACAGTCTTCCAGG
GTCCTCTCCTGTCCACCAACCGGGAGCCTCCACCTTGGCCATCCGTGAGCTATGAATGGCTT
TTTAAACAAACCCACGTCCCAGCCTGGGTAACATGGTAAAGCCCCGTCTTACAAAAAATC
CAAGTTATCCGGGCGAGGTGGTGTCGACCTGTAGTCCAGCTGCGAGTGGGCTGAGGTGGAG
GTGGAGTGGGGGGTGGGAGTGGAGGAGGAGTGCCTTGAGCCTGGGAAGTCGAGGCTGCG
AGTGAGCTGAGATTGCACACTGCAGCTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCAAAA

FIGURE 256

MSCVLGGVIPLGLLFLVCGSQGYLLPNVTLLLEELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYIMVSAGSGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GG SRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:**Signal peptide:**

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATGGG**
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCTCCTTGGCAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTCTGACAAATTCCTCCTATGAGTCCAGC
TTCTTGGAATTGCTTGAAAAGCTCTGCCTCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACAT**TCA**CAGCCATTGAAGCCTG
TGTCCCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCTGTCTTT
CAGCAGGCCCCACCTCCTGAGTGGCAATAAATAAAATTCGGTATGCTG

FIGURE 259

AATTGTATCTGTGTAATGTTAAAACAAACGAAATAAAATAGAAGGAAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTTCCTCCCTCC
CTCCGATTGTTCTAAATAAATTGAAAGATGCTGCTGTGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCTTGAAGCCAATGGAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGCTGTATTCATAAATTATATTTTGGGCTATCAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGTAAATGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTGTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCTGTTCCCTTGCAGCTTTTCTGCCCCCGCCAGCTGTAC
 CCAGGAGCCAGCCATGGTGCATTACATCTACCAGCGCTTTCAGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACGAGGGCATACATTCAAGAATTCAGAGATTCTCAAAAAATATA
 TCTGTTCATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCAGTGAAGAGTTGAACGTGCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACATGCTGATGGGCATAAAGTC
 TTTGAAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAAGATGCTGTCTATA
 ACTCTCAAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCATTTCATGGAGGATAACACCAAGCCAGCTCCCCGGAAGCAAACTCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATAAACCTGCGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCAATCTGGGCCAGGCCATAGCCATTGTTGTTCTCA
 CAAAGATTGAGCCGGGCACACTGGGAGTGGAGCATTTCATGGGATACCCCATGCGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGGTCTCTATGTGGTCTACAGTACTGGGGGCCA
 GGGCCTCATCGCATCACCTGCATCTATGATCCACTGGGCATCTAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACCTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCGTGAATGAAGGAACAGATCATTACAACTCCAGACAAAGAGAAA
 GCTGCCCTGTAAGTAAATGTCATTACAGCTGTGAGAAAGAGCACTGGCTTTGGCAGCTGTTCT
 TACAGGACAGTGAGGCTATAGCCCCCTTCACAATATAGTATCCCTCTAATCACACAGGAAG
 AGTGTGTAGAAAGTGGAAATACGTATGCCCTCCTTTCCCAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGGATGACCACATTCTGATACAGCCTACTTCAAGCCTTTGTGTTTACT
 GCTCCCCAGCATTTACTGTAACCTCGCCATCTTCCCTCCCACAATTAGAGTTATGCGCAGC
 CCCTAATATTACCACCTGGCTTTTCTCTCCCTGGCCTTTGCTGAAGCTCTTCCCTCTTTT
 CAAATGCTATTGATATCTCCCATTTTCACTGCCCAACTAAAATACTATTAATATTCTTTT
 CTTTCTTTTCTTTTTTTTGAGACAAGGTCTCACTATGTTGCCCAGGCTGGTCTCAAACCTCC
 AGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAATACTATTTCTTATTGAGGTTTAACTCTATTTCCTTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAATAATTAACATTGAAATATCGCTTT
 CCAGTGTTGGAGTGTGTCACATCATGAAATTCCTGTTTCACTTTGTGAAACATGCACAAG
 TCTTTACAGCTGTCACTCTAGTGATTTAGGTGAGTAACACAATTACAAGTGAAAGATACAGC
 TAGAAAACTACTACAAATCCCATAGTTTTCCATTGCCCAAGGAAGCATCAAAATCGTATGTT
 TGTTCACCTACTCTTATAGTCAATGCGTTTCATCGTTTCAAGCTAAAAATAATAGTCTGTCC
 TTTAGCCAGTTTTCTATGCTGCACAAGACCTTTCAATAGGCCTTTCAATGATAATTCTCTC
 AGAAAAACAGTCTAAGGGTGAGGACCCCAACTCTAGCCTCCTCTGTCTGTCTGCTCTGT
 TTCTCTCTTCTGCTTAAATTAATAAAAGTGACACTGAGCAAAAAA

FIGURE 262

MMVALRGASALLVLFLAAFLPPQCTQDPAMVHYIYQRFVLEQGLEKCTQATRAYIQEFQE
FSKNISVMLGRCQTYTSEYKSAVGNLALRVERAQREIDYIQYLREADECIVSEDKTLAEMLL
QEAEKEKKIRTLNASC DNMLMGISLKI VKKMMDTHGSMMDAVYNSPKVYLLIGSRNNTV
WEFANIRAFMEDNTKPAPRKQILTL SWQGTGQVIYKGF LFFHNQATSNEI IKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLT KIEPGTLGVEHSWDT
PCRSQDAEASFLLCGVLYVVYSTGGQGP HRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQIYAWNENQIIYKLQTKRKLPLK

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FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWL RAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFS PDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSD TTVLIWSLKGQVLSTINTNQMNNTHA AVSPCGRFVASCG
FTPDKVWVEVCFGKKGEFQEVVRAFELKGHSA AVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGA APCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGH LKRASNESTRQRLQQQLTQ
AQETLKS LGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCTTCACCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCTGTGAGCGGGATGTCCAGTGT
 GGGGCGAGCACCTGTGTGCCATCAGCCTGTGGCTTCGAGGGGTGCGGATGTGCACCCCGCT
 GGGGCGGAAGGCGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCTTCTTCAGGAAACGCA
 AGCACACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCGCGGACGGCAGGTAC
 CGTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTATTTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTCTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTCCCCCTCCCCTCCCAGGTGACCTGCTCTCTTCTCCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCTCGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTACAGCCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTGTGAGGCCCTCTTACCACACTTACCAGT
 TAACCACTGAAGCCCCCAATTCCCACAGCTTTTCCATTAAATGCAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTCCA
 AGGATCAGCCCTGAGAGCAGGTTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGGCTGAAAGGGGCACTGATTACAGACCAGGGAGG
 CAACTACACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEETCHP
GSHKVPFFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

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FIGURE 267

AGCGCCCGGCGTCGGGGCGGTAAAAGCGCGCAGAAAGGGAGGCACTGAGAAATGTCTTTC
 CTCCAGGACCCAAAGTTTCTTACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAAA
 GCAAAGGAGCTATGGGAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTATCCGTCTGGGAGTGTGGTACAACCTTCTCCGAGCCTGGAACGGAG
 GCTTCTCTGAAACCTGGAAGGAGAAGGCTTCATCCTTGGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGCACCAGAGAAAAAGAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACCACAGACTTTGGCCCTCAGAGAAAAATGAT
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTTCATGGGATGTATT
 GTTTCCTACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTTACTCTCAGTATGGATTA
 TTAATGTATTTAATATTCTGTTTAGGCCCTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTGCGGAGTTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCACTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLLANTDVFLSKPQKALEYLEDIDLKTEKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGWYNFFRAWNGGFSGNLEGEFGILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

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FIGURE 269

ACGGACCGAGGGTTTCGAGGGAGGGACACGGACCGAACCTGAGCTAGGTCAAAGACGCCCG
GGCCAGGTGCCCCGTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
AGCCCCCTTCTCGGCCTGCCCAACCCGCCACCCAGCCCATGGCGAACCCCGGGCTGGGGCTG
CTTCTGGCGCTGGGCCTGCCGTTCTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCTTCATCCACCACTCCAGCTCCGATG
GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
CTCCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
CACCTACCGGCCAGTAGCGAGGAGCAGTTCCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATCTAGGTCCCCCTCTCCTGCATCTGTCTCC
CTTCATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCCTGAGGTCAAGAGAGGATGGG
GCTATTCACTTTTATATATTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAAAA

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FIGURE 270

MANPGLG L L L L L A L G L P F L L A R W G R A W G Q I Q T T S A N E N S T V L P S S T S S S S D G N L R P E A I T A I I V
V F S L L A A L L L A V G L A L L V R K L R E K R Q T E G T Y R P S S E E Q F S H A A E A R A P Q D S K E T V Q G C L P I

MANPGLG L L L L L A L G L P F L L A R W G R A W G Q I Q T T S A N E N S T V L P S S T S S S S D G N L R P E A I T A I I V
V F S L L A A L L L A V G L A L L V R K L R E K R Q T E G T Y R P S S E E Q F S H A A E A R A P Q D S K E T V Q G C L P I

FIGURE 271

AATATATCATCTATTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTGGGTT
TTGGGATTTTAAATTTTCAAACACAGCAGAAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTGGAGATCCAATTCAGGAAGCAACACATTGGAGAATGGCTACTTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCCTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAA

FIGURE 273

GCCAGGAATAACTAGAGAGGAACA**ATG**GGGTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCTGCTGCAACAGTCAAATCTTCTTCATTAAAGCTGAAATTAATAGGCTTTGAAGATA
 TTGTCTATGTTTATAGATCTTACAGTGTGCCAGAGATGAAAAAATTAATGGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACTCTGTTTGAAGCCACAGAAAAAGATTTTTCACAAAA
 TGTATCTATATTAATCTCTGAGAATTGGAGGAAAAATCTCAGTACAAAAGGCCAAAAACATG
 AAAACCAATAACATGCTGATGTTATAGTTGCACCACCTACACTCCAGGTAGAGATGAACCA
 TACACCAAGCAGTTCACAGAATGTGGAGAGAAAGGCGAATACATTCACTTCAACCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCACAGGCCAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTCTACCGGTCTAAG
 TCAAAAAAATCGAAGCAACAAGGTGTCCCGAGGTATCTCTGGTAGAAATAGAGTTTATAA
 GTGTCAAGGAGGCAGCTGCTTCTTAGTAGCATGCAGAAATTGATTTCTACAACAAACTGTATG
 GAAAAGATTGTCAATCTTCTCTGATAAAGTACAACAGAAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTCTGTTGTTGAATTTTGTAAACGAAAAACCCATAATCAAGAAGCTCCAAG
 CCTACAACACATAAAGTGCAATTTTAGAAGTACATGGGAGGTGATTAGCAATTTCTGAGGATT
 TTA AAAACACCATACCCATGGTGACACCACCTCCTCCACTGCTTCTCATTTGCTGAAGATC
 AGTCAAAGAAATTTGTGTGCTTAGTTCTTGATAAGTCTGGAAGCATGGGGGGTAAGGACCGCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACTGTTGAAAAATGGATCCTGGG
 TGGGGATGTTTCACTTTGATAGTACTGCCATATTGTAATAAGCTAATCCAAATAAAAAGC
 AGTGATGAAAGAAACACACTCATGGCAGGATTACCTACATATAGCTTCTGGGAGGAACTTCCAT
 CTGCTCTGGAATTAATATGCAATTTCAAGGTGATTGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGATGGGAGGAGTAACTGCAAGTTCTGTGATTGATGAAGTG
 AACCAAAAGTGGGGCAATTTGTTCAATTTTATGCTTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGATGAGCAAGATCAAGGAGGAAAGTCAATTTTATGTTTTCAGATGAAGCTCAGAACAATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCAGCAAGTCCCTT
 CAGCTCGAAAGTAAAGGATTAACACTGAATAGTAATGCCCTGGATGAACGACACTGTCAATAT
 TGATAGTACAGTGGGAAAGGACACGTTCTTTCTCATCAGTGAACAGCTGTGCCTCCAGTA
 TTTCTCTCTGGGATCCCAAGTGAACAAATAATGGAATAATTCACAGTGGATGCAACTTCCAAA
 ATGGCCTATCTCAGTATTCAGGAACCTGCAAGAGTGGGCACTTTGGGCATACAATCTTCAAGC
 CAAAGCGAACCAGAAACATTAACATTTACAGTAACTTCTCGAGCAGCAAACTTCTTCTGTC
 CTCCTCAATCAGCTGAATGCTAAATGAATAAGGACGTAAACAGTTTCCCCAGCCCAATGATT
 GTTTACGCGAAGTTCTACAAGGATATGTACCTGTTCTTGGAGCCAACTGTGACTGCTTTCAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATAATGGTGACGGCGCTGATT
 CTTTCAAGAAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAGTTTCGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAATTTACGGCTCCACT
 GAATAGAGCCCGGTACATACAGGCTGGGTAGTGAACGGGGAATTTGAAGCAAAACCGGCCAA
 GACCTGAAATTTGATAGGATACTCAGACCACCTTGGAGGATTTACGGCGAACAGCATCCGGA
 GGTGCAATTTGGGTATCAAGACTCCCAAGCCTTCCCTGCGTGAACCAATACCCCAAGTCA
 AATCAGACACCTTGATGCCACAGTTCATGGAGGATAAGATTAATTTTACATGGACAGCAGTCA
 GAGATATTTTGTGATTTGGAAAAGTCAACGTTATATATATAAGAAATAGTGAAGTATTTCTT
 GATCTAAGAGCAGTTTTGTATGATGCTCTTCAAGTAAATACTACTGATCTGTACCAAAAGGA
 GGCCAACTCCAAGGAAAGCTTTTGCAATTAACCCAGAAAATATCTCAGAAGAAAATGCAACCC
 ACATATTTTATGCCATTAAGAGTATAGATAAAGCAATTTGACATCAAAAGTATCCAACATT
 GCACAAGTAACCTTTGTTTATTCCTCAAGCAAACTCTGATGACATTTGATCCTTACCTACTCTC
 TACTCCTACTCCTACTCTCTGATAAAAGTCATAATTTCTGGAGTAAATATTTCTACGCTGTAT
 TGCTGTGATTTGGGCTGTTGTGAATTTGTTAACTTATTTTAACTACCACTTTGAACCTTGA
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAAAACCAACAAATGTAAAT
 AAAGGATATTTCTGAATCTTAAATTCATCCCATGTGTGATCATAACTCATAAACATAATTT
 TTAAGATTCGCGAAAAGGATACTTTGATTAATAAAAAACACTCATGGATATGTAACAACTGT
 CAAGATTAATTTTAAATAGTTTCAATTTATTTGTTATTTTATTTGTAAGAAATAGTGATGAAC
 AAAGATCACTTTTTTCATAGTACCTGGTGTATATTTATTTGATGCAACAGTTTTTCTGAAAT
 GATATTTCAATTTGCATCAAGAAATTAATATCATCTATCTGATGTCAAAATACAAAGTAAA
 GGAGAGCAAAATAAACACATTTGGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA
 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDPSVPEDEKIEQIEDMVTTASTY
 LFEATEKRFFFKNVSIILIPENWKENPQYKRPHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GEKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVFDEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSGLSRACRIDSTTKLYGKDCQFFPDVKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRLNRMNQAACHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLTLDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPPSISLWDPSTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTIITVTSRAANSSVPPITVNAKMKNKDVNSFPSPMIVYAEILQG
 YVPVLGANVTAFIESQNGHTEVLELLDNGAGADSFKNQDGVYSRYFTAYTENGRYSIKVRAHG
 GANTARLKLRLPLNRAAYIPGWVNGEIEANPPREIDEDETQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTATVHEDKIILTWAPGDNFVDGKVGQRYIIRISASILDRLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIQAQVTLFIP
 QANPDDIDPTPTPTPTPDKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

FIGURE 275

CTCCTTAGGTGGAACCCCTGGGAGTAGAGTACTGCAGCAAAGACCGGGAAGACCATACGTCCTCCCG
 GGCAGGGGTGACAAACAGGTGTGATCTTTTTGATCTCGTGTGGGTGCCTTCTTATTTCAAGGAAAG
 ACGCCAAAGTAAATTTGACCCAGAGGAGCAATGATAGGCCACCTCTCTAACCTTCCCTTTCTTGAACC
 CCGAGTTATGCCAGGATTTACTAGAGAGTGTCAACTCAACCAGCAAGCGGCTCCTTCCGGCTTAACTCT
 GTGGTTGGAGGAGCAACCTTTGTGGGGTGCCTTCTCTTAGCAGTGTCTCAGAAGTGACTTGCCTTGA
 GGGTGGACCAAGAAAGAAAGAGGTCCCTCTTGCTGTTTGGCTGCACATCAGGAAGGCTGTGATGGGG
 AATGAAGGTGAAAACTTGGAGATTTCACCTCAGTCATTGCTTCTGCTGCAAGATCATCTTTAAAAA
 GTAGAGAAGCTGCTCTGTGTGGTGGTAACTCCAAGAGGCGAGAATCCTGTCTAGAAGGAAATGGATG
 CACGAGCTTCCGGGGGCGCCAAACGCATGCTTCTGTGCTTAGCCACGGGAAGGCCCTTCCGTGGGG
 GCGCGGCTTCCGGGGATGCCACGGTTCTGGACGCATGGCTGATTTCTGAATGATGATGGTTCCGC
 GGCGGCTGCTTGGGATTTCCGSGGTGGTGGTTTGTCTGTCTGCTCTCTGCTGTCTCTCTCTCT
 CCTGTACATGTTGGCTGCACCCAAAGGTGACGAGGAGCGCTGGCATTGCCACGGGCGCACAGC
 CCAACGGGGGAAGGAGGGGTACACGGCCGCTCCTTCAGGAGTGGGAGGAGCAGCACCGCAACTACGTGA
 CGACCTTGAAGCGCAGATCGCACAGCTCAAGGAGGAGCTGCAGGAGAGAGTGAGCAGCTCAGGAA
 TGGGCAGTACCAAGCCAGCAGTGTCTGTGGCTTGGCTTGGACAGGAGGCCCCAGAGAAAACCCAG
 GCGACCTCTCTGGCCTTCTGTCACTCGCAGGTGGACAAGGCAGAGGTGAATGCTGGCGTCAAGTGG
 CCACAGAGTATGCAGCAGTGCCTTTCGATAGCTTTACTCTACAGAAGGTGTACCAGCTGGAGACCTGG
 CTTTACC CGCACCCGAGGAGAAGCCTGTGAGGAAGGACAAGCGGGATGAGTTGGTGAAGCCATT
 GAATCAGCCCTTGAGACCTTGAACAATCCTGCAGAGAAGACGCCCAATCAGCGCTCTTACACGGCCT
 CTGATTTTCATGAGGAGGCTATCCGAAACAGAAAGGACAAGGAGCACTTGTATGAGCTACCTTTCAA
 AGGGAGCCACAAACAGCAATTTCAAACGGCTCATCTTATTTGACCACTCAGGCCCACTGAAAGGTG
 AAAAAAGAAAGCTCAACATGGCCCAACAGGCTTATCAATGTTATCTGTCCTTCAGCAAAAAGGGTGG
 ACAGTGTCCGGCAGTGTCTGCAGAAATTTTCAGGGAGATGTTCATTCAGCAGATGGAGGAGCTATCT
 CTCTGTGTTTCTTGGGACATGCAAGAAATCAAGAAATCAAGAAATCAAGAAATCAAGAAATCAAGAA
 CTGGCAACTTTCAGGAATTTTACCTTCTACCTGAAATGGAGAATTTCTCGGGGAAGGAGCACTTG
 ATGTTGGAGCGCGCTTCTGGAAGGGAAGCAACGTCCTTCTCTTTTCTGTGATGPGGACATCTACTT
 CACATCTGAATTCCTCAATACGTGTAGGCTGAATACACAGCCAGGGAAGAAGTATTTTATCCAGTT
 CTTTTCAGTCAGTACAATCCTGGCATAATATACGGCCACCATGATGCAGTCCCTCCCTTGGAAACAGC
 AGCTGGTCATAAAGAAGGAAACCTGGATTTTGGAGAGACTTTGGATTGGGAGCTAGCTGTCAAGTCTG
 GTCAGACTTCATCAATATATAGTGGGTTGATCTGGAACATCAAAGGCTGGGGCGGAGAGGATGTGCAC
 CTTTATCGCAAGTATCTCCACAGCAACCTCATAGTGGTACGGACGCCGTGTGCGAGGAGATCTTCCACC
 TCTGGCATGAGAAGCGCTGCATGGACGAGCTGACCCCGGAGCAGTACAAGATGTGATGTCAGTCCAA
 GGCCATGAACCGGCGATCCACGGCCAGCTGGGCTGCTGGTGTTCAGGCACAGATAGAGGCTCAC
 CTTTCGCAACAGAAACAGAAAGCAAGTAGCAAAAAAAGCACTCACTCCACAGAGAAGGATTTGTGGGAGA
 CACTTTTTCTTCTTTTGCATTAATCTGAAAGTGGCTGCACAGAGAAGAACTTCCATAAAGGAGC
 ACAAAAGAAATTTGACTGATGGTGCAGAGATGAGAAGCTCCGATTTCTCTGTGTGGCTTTTAC
 AACAGAAATCAAATCTCCGCTTTCGCTGCAAAAGTGAACCCAGTTGCATCTGTGAAGTGTCTGACA
 AAGGCAAGTGTGTTGTGAGATTATAAGCCTAATGGTGTGGAGGTTTACCTGTGTTTACAATACAT
 GAGACCTGTTGTTTGTGTGCTCATTGAAATATTCATGATTTAAGAGCAGTTTGTAAAAAATCACT
 TAGCATGAAAGCAAGCATATTTCTCTCATATGAATGAGCCTACAGCGGCTCTAGTTTCTTAGG
 AATGCTTAAAAATTCAGAAGGCGAGGAGAGATAGGCTTATTTATGATACTAGTGAAGTACATTAAAGA
 AAATAAAATGGACCAAGAAAGAAAGAAACATAAAATATCGTGTATATTTTCCCAAGATTAACCA
 AAAATAATCTGCTTATCTTTTGGTTGTCTTTTAACTGTCTCCGTTTCTTTCTTTTAAAAAT
 GCACTTTCTTCTTGTGAGTTATAGTCTGCTTATTTAATTACCATTTCGACGCTTACAAGAGA
 GCACAAGTTGGCTACATATTTATATTTTTTAAAGAGATACCTTGAGATGCATATGAGAATTTCA
 GTTCAAGAGCATAAATGTATGCCATATCCAAAGCATGCCAAATGCTGCTGTCAGGCACATGAAT
 GTCAAGCATGCAACATGAGCAAGAAAGTGTGTTCTACTATACAGACCTTACAGATATCTTCTGAA
 GACTATTTCCAGAGAGGACACTGAACACTGGAGGAAGAAAGGACATTTCTGTTTACAGAA
 AAGGAACATCTCAGACTGGTGATATCGTGATGTACCTAAAAGTCAGAAACACATTTTCTCTCA
 GAAGTAGGAGCGCTTCTTCACTGTTTAAATAAACCAAGTATACCGTGTGAACCAACACATCTCT
 TTTCAAAACAGGCTGCTCTCTGGCTTCTGGCTTCCATAAGAAGAAATGGAGAAAATATATATAT
 ATATATATATATTTGAAAGACTCAATCCATCTGCCAGATCTAGTGGGATGGAAGTTTGTGCTACAT
 GTTATCCACCCAGCGAGGTGGAAGTAACCTGAATTTTAAATAAGCAGTTCTACTCAATCA
 CCAAGATGCTCTGAAAATTCGATTTTATACCATTTCTCAACTATTTTAAAAAATAATACAGTA
 ACATAGAGTGGTTTCTTCACTCATGTGAAATTTATAGCCAGCAGCATGCTAGTGATTAATCT
 CTTTGTAGTCTGCTTCTGTTTGTCTCAGTAACCTCATTTGTTTAAAAGCTTCAAGAAAGCTCAAG
 TGTGGTGTGTTAAAAAATGCATGTATTGATTTGTACTGGTAGTTTGTGAATTTTAAATAAACAC
 AGGCCATGAATGGAAGGTGGTATGCACAGCTAATAAAATATGATTTGTGGATATGAA

FIGURE 276

MMVRRGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAVPFDSFTLQKVYQLETGLTRHPEEKPVKDKRDELVEAIES
ALETNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVKNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYPVLFSEQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDDIKGWGGEDVHLYRKYLHSNLIVVRTPVRLFHLWHEKRCMDLTPEQYKMCMQS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSSKKT

FIGURE 277

GAAAGAATGTTTGTGGCTGCTCTTTTCTGGTGACTGCCATTATGCTGAACCTCTGTCAACC
 AGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCTTCTCTGCTGTTGAGGTGC
 AATCAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAACT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGCACCACCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACACTGATTATTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTCTCTTCTCAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTTCTTTGTAATAAAATTTGAATGTGCT
 TGAAAGTGAAAAGCAATCAATTATACCCACCAACACCACTGAAATCATAAGCTATTCACGAC
 TCAAAATATTCTAAATATTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCTTTTTGACGATCACTTATATCACTCTGTATATGACTAAGTAACCAAAAG
 TGAGAAGTAATTATTGTAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCTCTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCCTAATAGGAC
 AATTCTATTGTGACCATTCTACAATTTGTAAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTL
FLKIPSTLAPPMDSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

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FIGURE 279

AACTCAAACCTCCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTCATGT
 ATGGCAAGAGCTCTACTCGTGGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGAAATTTATACCTCCCGGGTCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACCTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGGA
 ATTTTCGTCTCTAGACGGGGGACCTGAGCAGTTTGATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCTCGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGACTAAACAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACAA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAAACAAGAAGCTACATTTTGCCTTAA
 GACACTACTTACAGTGTTATGACTTGTATACACATATATTGGTATCAAAGGGGATAAAAGCC
 AATTTGTCTGTTACATTTCCCTTTCACGTATTCTTTTACGAGCACTTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTCTCCACATTCTCAATTAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAAACAGTAAATCCTAAATCAAACCTGTTAAATGACATTTTTATTTTTATGTCTC
 TCCTTAACATATGAGACACATCTTGTTTTACTGAATTCTTTCAATATTCAGGTGATAGATT
 TTTGTCTG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSSFAPVGDALTVT
WNFRPLDGGPEQFVFYHIDPFQPMSEGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNPPDVGIVIGEIRLSVVHTVRFSEIHFLALAIGSACALMIIIVVVVLFQHYRKKRWAER
AHKVVEIKSKEERLNQEKKVSVYLEDTD

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70
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100
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GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACC**ATGA**AGTCTTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCTGTCTGATGATGAAGCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCTACCACTGCAACCAACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCAGTTTACCCAAATGGGTGGGGATCTCCCGAATGGTAGAGTGTGTCCCT**T**
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTTCA
ATCAAACACTACTACCTTGCCTACGATATCCCCCTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGCTGCAACATCAAAAAA

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FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
CTAGGGGTCTGGATTTGCTGGTTAAACAAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCTGGTCCCTCCTTGCCGAGAGA
GTGTCCTGGGTGAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGCCAGTCCAGGGTGGGGGGCG
GCAAACCTCCATAAAGAACCAGAGGGTCTGGGCCCGGCCACAGAGTCATCTGCCAGCTCCT
CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAACACAGGCTGG
ATTTGCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
CCCCAAGAGCTTTCATTGTATCTATTGATTTTTACCACATTAGCAATTAACCTGAGAAAT
GGGCCGGGCACGGTGGCTCACGCCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA
TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
GCAGGAAAATCGCTTGAACCCAGGAGGCGGACGTTGCGGTGAGCCGAGATCGCGCCGCTGAT
TCCAGCCTGGGGCACAAGAGTGAGACTCCATCTCACACA

FIGURE 285

GTCAATGCCAGTGCCTGCTCTGTGCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
CGGGCCCCCATGGGCGGCCAGAACTGGCACAGCATGAGGAGCTGACCTGCTCTTCCATGG
GACCTGTCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
AGGCCAGGAACAGCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTGAGC
CGGGGCCGGGATGCAGCCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
AGATCCAGGAGAGACTCCACACAGCGGCGCTCCCAGCCTGAATCTGCCTGGATGGAATGAG
GACCAATCATGCTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
CCTGTTCACTGGGATCAGCCAGGGCGCCGGGCCCACTTCTGAGCACAGAGCAGAGACAGAC
GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTGGGGAGGGGTGGAGGAAGGACATGTA
CCCTTTCATGCCTACACACCCCTCATTAAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRREMVAQQHRLRQ
IQERLHTAALPA

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FIGURE 287

GGCAACATGGCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAATTTGCAT
 CCTGGTGATCACCTTACTCTGGACCAGACCACCAGCCACACATCCAGATTAAAAAGCCAGGA
 AGCAGAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTTACAAGAAATGCTACCTTGCTTCAGAAGGTTTGAAGCATTTCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGTACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAGCGAGAAAACCTGTGTCCTGTTCTCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTCGACGACGACAAGAGATACATATGCGAGTTCACCATCCC
 TAAATAGGTCTTTCTCCAATGTGTCTCCAAGCAAGATTATCATAACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATTTGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGCTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGCT
 AAACAGACTAAAATCTTCTCTCTAGTCTTTCTCACTTGTACAAACCCAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCCTTGGAAGTTTAGCGTATGTTTGACTAACAAAAATCCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAAACTTTTCAGCCTGTTGCTCATCTGTCCTCCATGCTGGCAATAATACC
 TTGTGAGCCCATACCTTATTTTGAATTGCTCCATCTCTGGTGGGACTTGATCTTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTTCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGACTTACATTTCCTTTTTTACATTT
 TCGTATATTTATTTTTTTTAGCCATCATTTATATGTTTAAAGTCTATATGAGGCAACCAATCTT
 TGGAAGCTGAAAACGAATTTAAAGAATGCTATCTTGGAATAATGTCATACGCTCTGTGCAATT
 TTTTATTCTGCCTAGTGCTATTCTGCTTGTTTAACTAGATTGTACAAAAATAACTTCATTGCT
 TAATATCAAATTACAAAGTTTAGACTTGGAGGGAATGGGCTTTTTAGAAGCAACAATTTT
 AAATATATTTTGTCTTCAAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTAACTACACATGCTTGAATTAAGTTTGTAGCTGTTTTCATTGCTCA
 ATAATAAAGCCTGAATTCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGLKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRS LPGVND FWL GINDM VTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQ GK
WSDEACRSSKRYICEFTIPK

FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGCAGCTGAAGGGAGGCAT
 CCTTGGCCTCCGCAGCCGATCAC**ATGA**AGGTGGTGCCAAGTCTCCTGCTCTCCGTCTCTCTG
 GCACAGGTGTGGCTGGTACCCGGCTTGGCCCCCAGTCTCTCAGTTCGCCAGAGACCCCGAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAGCCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGGATTACGCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCTCCATTTGGCATGTCTTGGCCATGCACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGGCCCTGAAGCCCCACCAAG
 CCCGGGCTCTGCTTCCCTCTTTAAGGGACTCAGAGAGACCCCTCTCCGCAACCTGGAAGT
 GGGCTCTCACAGGGGAGTTTTGCTTTCATCCACAAGGATTTTGATGTCAAAGAGACTTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTAACAAAGAGACTCGGGGGAAAATTTCCAAACT
 GTTTGATGAGATTAATCCTGAAACCAATTAATCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCATTGACCTGTCTTACCAGAAGTCGACACTTTCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCTCCACCTTTGACAAGAA
 TTTTCGTTGTCTCTCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCTCA
 TGGAGAAAATGGGTGACCACTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAACCCAGAAACATGGAAGTTTTCTTTCCGAAGTTCAAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAAGAATCTTCTCACCCCTTTG
 CTGACCTTAGTGAACCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTGAGAAATTAAG
 TGCTTATTCATGCTCTCTGTCTCATCAAAGTGGACCGCCATTTTCATTATGATCATGTAAG
 AAACCTCTGGAATGCTTCTGTTTTCTGGGAGGGTGGTGAATCCGACTCTCCTAT**TAA**TTCCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTCTCTTTGTTCTTAACTAGTTTTAGGGTGTCTC
 AAATAAATACAGTAGTCCCACTTATCTGAGGGGATACATTCAAAGACCCCAAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAATTTATAAATTAGGCACAGTAAGAGATTAAACAATAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACTTGGGCAAGGGGAGAATTCA
 CATCTGGGTGGGACAGAGCAGGACGATGCAAGATTCATCCCACTACTCAGAATGGCATGC
 TGCTTAAGACTTTTAGATTGTTTATTTCTGGAATTTTCATTTAATGTTTTTGGACCATTGGT
 TGACCATGGTTAACTGAGACTGCAGAAAGCAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAATTTGATACATATTTTTTAAAAA

MKVVP S L L S V L L A Q V W L V P G L A P S P Q S P E T P A P Q N Q T S R V V Q A P R E E E E D E Q E A S E E K A G E
 E E K A W L M A S R Q Q L A K E T S N F G F S L L R K I S M R H D G N M V F S P F G M S L A M T G L M L G A T G P T E T Q I
 K R G L H L Q A L K P T P K P G L P S L F K G L R E T L S R N L E L G L S Q G S F A F I H K D F D V K E T F F N L S K R Y F
 D T E C V P M N F R N A S Q A K R L M N H Y I N K E T R G K I P K L F D E I N P E T K L I L V D Y I L F K G K W L T P F D P
 V F T E V D T F H L D K Y K T I K V P M M Y G A G K F A S T F D K N F R C H V L K L P Y Q G N A T M L V L M E K M G D H L
 A L E D Y L T T D L V E T W L R N M K T R N M E V F F P K F K L D Q K Y E M H E L L R Q M G I R R I F S P F A D L S E L S A
 T R N L Q V S R L R R T V I E V D E R G T E A V A G I L S E I T A Y S M P P V I K D R P F H F M I Y E E T S G M L L F
 L G R V N P T L L

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAAGCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCACTGGTGGTGTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCCTGGGCCGTGTCCTGAGTCCC
GAGCCCAGCCATGACAGCCTGTACCACCCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGCC
CCGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCCACA
TCTACCACCCCAGTAGGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
AAAAAAAAAAAAAAAA

FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
TACCCAAGGAAAAGTGCAGCTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTGC
TGTTTCTCATAGCGACCACCAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
TGGACCTGTTCTTCGCTCTCCATCTCTGCCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
TAGTGCAATTGATGGCTGTATTTTCTCCGCACTGAGAATGGTGTATCTACCAGACCTTCT
GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
CGTGGGAAGTGCACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
CCCAATAAGTCCCCCATGCAGCACTGGAGAACAGCTCCCTGCTGAGGTACCGCACGGACAC
TGGCTTCTCTCCAGACACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAAT
ATGGAGAAGGAAAAGTGTGGACTGACAACGGCCCCGGTGATCCCTGTGGTCTATGATTTTGGC
GACGCCAGAAAACAGCATCTTATTACTCACCTATGGCCAGCGGGAATTCACTGCGGGATT
TGTTCAGTTCAAGGTATTTAATAACGAGAGAGCAGCCAACGCCCTTGTGTCTGGAATGAGGG
TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
CCCCAGCAGTGTGGAGATTTTCTGGTTTTGATTGGAGTGGATATGGAATCATGTTGGTTA
CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
GGAGGGAACCCAGACCTCTCTCCCAACCATGAGATCCCAAGGATGGAGAACAACCTTACCCA
GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
GVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANYNTFG
SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYQGREFTAGFVQFRVFNNERAAN
ALCAGMRVTGCNTEHHCIIGGGGYFPEASPQQCGDFSGFDWSGYGTHVGYSRSSREITEAAVLL
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FIGURE 297

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGGGACTCGGCGCGCGAGGTGCTTGGGCCG
 CGTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAAAACATAGAGAATTCTGGGCTTCCACACAACCTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTTCACTGACATCTGCTGCTTCATCAGTAACAATCACAACAATATGCAT
 TCTGAAGCAAAGAAAGGATCAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAAC
 GCTGGGAGTTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTTAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTTCT
 CTTTTTGAAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCCTCAAGGTAACAAGGGTTTGGGTTTGAATAAACAATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTCAGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTTGGTCACATATGACCAGTAATTGAAAGACGTCATCACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGT
 AGCTCACATAAAGAAGTTTCACTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACCTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTG
 TGCTTTAAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

MGLGARGAWAALLLGLQLVALLLGAHESAAMAASANIENSGLPNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVTMTKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTVTHNSSVTSAASSVTITTTMHSEAKKSGKFDTGSEFVGGIVLTGLVLSILYIG
CKMYYSRRGIRYRTIDEHDAII

FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCGAGCCGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGCATGCGCACCCTGTGGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTCTGCCTGGCGCTTTCCTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAATTTTCGAGGATGTCAGATGTAATGTATCTGCCCTCCCT
 ATAAAGAAAAATCTGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGTCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCAAAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACAGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGAGCGCTGGAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTCTTTGACCGG
 CATGTTGTCTCAGCTAATGGGAATTGAATTCAGGTTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAAGAACTGACTGGGTTTTGCTGGGTTTTCAATTTTAATACCTTGTGATTTTACCAACT
 GTTGCTGGAAGATTCAAAACCTGGAAGCAAAAACCTTGCTTGATTTTTTTTCTGTAAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAAATAAGTCTTTTCTATTTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTTGGTGGGAGAGGGGAGGATGCCTGGGAAGTGTTT
 AACAACTTTTTTCAAGTCACTTTTACTAAACAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCAGTACTGTATTATCTGGGTATCTGCTGTGTCTGCACCTTCATGGTAAACGGGAT
 CTAAATGCCTGGTGGCTTTTCAAAAAAGCAGATTTTCTTCATGTACTGTGATGTCTGATG
 CAATGCATCCTAGAACAACTGGCCATTTGCTAGTTTACTCTAAAGACTAAACATAGTCTTG
 GTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAACTGGCTTTTT
 TCTTCTATGTCTCTTTTGAATGTAACAATAAAAAATAATTTTGAACATCAA

GCACCTGCGACCACCGTGTAGCAGT**CTAGG**CGGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
CTGGGCTTGTCTCTGGCTCTGTCTGCTGCTGCCAAGGCCTTCTGTCCCGCGGGAAGCGG
CAGGAGCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
CCAGGCACCTCAGATGGCCAGACTCTCTGGGCTCGTTTCCAGAGTCTCACCTTGCCGAGG
CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGAAGAGGTCG
ATGGGGCAGATTATTCGAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCATT
TAAGGTAAGTAGAATCATCCTAATCATATTACATCA**TGA**AAATCTAATATGGCGATAAAAA
TCATTGTCTACATTAAAACTTCTTATAGTTTCATAAAATTATTTCAATCCATCATCTCTTTA
AATCTCGCTCCCTCTTCTTACAGGTACTTAGGATAGCCATTATTTCAAGTTTCCACATAAGAAAT
TTTACTCAATGTTTAAAGTGTTTGCCCAAAATTCACAATCAACAGGCAGAACTAGGACT
GAACATGATCTTTTGGTCTTAAATCCAGTGAGTGATACAAATCAATGCATCCCTGCCA

FIGURE 302

MAYSTVQRVALASGLVLALSLLLKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
PGARFQRSHLAEEFAKAKGSGGGAGGGSGRGLMGQIIPIYGFIFLYILYILFKVSRILI
ILHQ

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FIGURE 303

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCCTCCCTGGGTGCTCTTCATCTT
 GGATTTGAAAGTTGAGAGCAGCATGTTTTGCCACTGAAACTCATCCTGCTGCCAGTGTTAC
 TGGATTATTCCTGGGCCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
 GGTGATTACGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
 AGACTGGACTCTGTCAACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
 ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCCTGACACTTGATGGGGGACATCTTATGC
 AATGATGGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
 AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAG
 AGGAGCCCCAAGAGCTCATGGTCCATGTGGTGGATTGATTGAGATGGGATGTGTTTTCCAG
 AGCAGAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGA
 GGAGATTGTATTTTCGTTACTACCACAAACTCAGGATGTCTGTGGAGTACTCCCAGAGCTGGG
 GCCACTTCCAGAATCGTGTGAACCTGGTGGGGGACATTTTCGCAATGACGGTCCATCATG
 CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
 GGTGTTCAAGAAAACCATTTGTGCTGCATGTGAGCCCGAAGAGCCTCGAACACTGGTGACCC
 CGGCAGCCCTGAGGCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTC
 TGTGCCACAATCCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
 GAGTTCAGTGAATTTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAG
 AAAAACCCTGCCATTTTGAAAGATGTGAAGGGGAGAAACATTTACTCCCCAATAATTGTA
 CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAATAATCAGAGGCCACCTACATGACCATGCA
 CCCAGTTTGGCCTTCTCTGAGGTGAGATCGGAACAACCTCACTTGAAAAAAGTCAGGTGGGG
 GAATGCCAAAAACACAGCAAGCCTTTTGAAGAAGATGGAGAGTCCCTTCATCTCAGCAGCGG
 TGGAGACTCTCCTGTGTGTGCTCCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
 CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
 CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
 CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCGCTT
 GGATCAGACCCCTCCTGTGGGCAGGGTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
 AAAACCAACCCCAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYSNLSVPIGRFQNRVHLMGDI LCNDGSILLQDVQEADQGT YICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLPV LILIVKKT CGNKSSVNSTV
LVKNTKKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNSLEKKSGGGMPKTQQAF

FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACATTTTGC AAAAGTCATTGAACCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTAAAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTGGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAACCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAAAAATCAGAACTAAAGGGCACTTTCAAGGTCATAATGCAGCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTAACATGGGAAGAGAG
 TAAGCAGTACTGCACCTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
 AGAACAAACATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

MQDEGDYITLNIKTRPALVSVPASSSWRVMALILLILCVGMVVLVALGIWSVMQRNYL
QDENENRTGTLLQQLAKRFQYVVKQSELKGTFKGHKCSPCDNTWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHLIRWGLSRQKSNEVWKWEDGSGVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCKERGAMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTCGCGCAGTTCTGCCTCCGCCTGCCAGTCTCGCCCGCGATCCCGG
CCCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
CGCCGGAGGAGCTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTCCGGAGAA
GCCCCGGCAAACGCAGGCTAAGGAGACCAAAGCGGCGAAGTCGCGAGACAGCGGACAAGCAG
CGGAGGAGAAGGAGGAGGAGGCCAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
CGTCGTGGCCATGGCGGCGGCTATCGCCAGCTCGCTCATCCGTAGAAGAGGCAAGCCCGCG
AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAAGGCAAGACCAGCTGC
GACAAAAACAAGTTAAATGTCTTTTCCCGGGTCAAACCTCTCGGCTCCAAGAAGAGGCGCAG
AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAAGATGAGGACAGCACTTACACT
CTGTTTAACTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
GTACTTGGCAATGAACAGTGAGGGATACTTGTACACCTCGGAACCTTTCACACCTGAGTGCA
AATTCAAAGAATCAGTGTGTGAAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGCCCATGT
ACAAGGAGCCATCACTGCAGATCTCACGGAGTTCTCCCGATCTGGAAGCGGGACCCCAACC
AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGGCAAAAGAAGGGCTCTGTAACAGAACCCTTACCTCCAGGTGCTGTTGAAT
TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTCAGTGACATTACCAAACAAACAGG
CAGAGTTCATATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGKTSCKDNKLNVSFVKLFSGSKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKEDSTYTLFNLIPVGLRVVAIQGVQTKLYLA
MNSEGILYTSELFTPECKFKESVFENYYVTYSSMIYRQQQSGRGWYLGLENKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKRSRSVSGVLNGGKSMHNEST
```

N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGGATTTCAGTGAAAAAGTGGGGGATCCCTT
 CCATTTAGAGTGTAGCAAAGGAAAAAACACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCCACACCTGTAGATTAC
 AAGAGTGGATTGTCAGGAGTGTGCCCCAAAATACAGTGGAAGGTGCCTGAAGATATTTAA
 ACCACGTCTTGGAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGAAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCCAGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCTATGCGCGCGCTGGC
 CAGTAGCCTGATCCGGCAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGCGCCGGTGTCCG
 CGCAGCGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGCTCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCGCGCGGCGGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTCTTCTGCCGCCAGGGTTTCTACCTCCAGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAAGCTCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCTCCGTGTGGTCACCATCCAGAGCGCCAAGCTGGGTCACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCCTGTACGCCTCTGCTCTCTACCGCCAGCGTCGTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTATGAAGGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCCACTTTCTGCCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCTCCCTTCCAGTCCCCCTGCCCTTGAATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTKSLCQKQLLILLSKVRLCGGRPARPDR
GPEFQLKGIVTKLFCRQGFYLOANPDGSIQGTPEDTSSFTHEFNLIIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGCGGAGCAGCCCCAGCAAGAACC GCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTAAAAACAGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAATAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGACCTGGTTTTTGGGATTAAATAAGGAAGGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCC GAAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCCTCTGCAATAATGAATGGAGGCAAACAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWRPSSASRRSSPSKNRGLCNGNLVDIFSKVRIFGKKRRLR
 RQDPQLKGIVTRLYCRQGYLQMHDPGALDGTKDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLYPSELFTECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTFSKSTSASAIMNGGKPVNKSSTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

GCGGAGGAGGAATTGACCATGTAAGAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
GAAGGATGCAGGAGCGAGCTTCTCCTGGAAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAGGAAGA
ACGAAGCTTTTTCTGTGAGCCCTGGATCTTATACACAAATGTGTATATGTGCACACAGGAGCATTCAAGATG
AAATAAACAGGAGTTAGACCCGCGGGTGGTGTCTGTGCATAAATAAAATCTTTAAAGAGCAGTGTCC
CTCCCACCCGCAAAAAGGATGATTGGAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTTCAATTT
TTCTCTATAAAGGAGAAAGTAGGCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTTAGTAAAGTAA
AGAACTGGTGTGGTGGTGTCTTCTTCTTTTGAAATTTCCCAACAGAGGAGAGAGAAATTAATAATACATCTCG
AAAGAAATTTAGAGAGAAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAACACGAGCAGCA
CAGTTGGATTTGTGCGAATGTTGACATAAAATGACGGATAATTCAGTTGGATTTTCTCATCAACCTCCTTT
TTTTAAATTTTATTCCTTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAACCACTCGGATTTCCATCT
GGATGTTGCTGTGATCAGTCTGAAATACAACCTGTTTGAATCCAGAAGGACCAACACAGATAAATATGAATG
TTGAACAAGATGACCTTACATCCACAGCAGATATATGATAGGTCTTAGGTTTAACAGGGCCCTATTGACCCCT
GCTTGTGGTGTCTGCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCCCTTCTGTGT
GCTCTCGCAGCAACGATTCAGCAAGGTGATTTGTGTCGGAACCAATCTCGTGAGTTCCGGATGGCATCTCC
ACCAACACACGGCTGCTGACAGCTCCATGAGAACCAATCCAGCATCAAGTGAACGCTTCAAGCATCTGAG
GCACTTGGAATCCTACAGTTGAGTAGGAACCATATCAGAACCATTGAAATTTGGGCTTCAATGGTCTGGCA
ACCTCAACACTCTGGAACCTCTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTTGATATCTTGTCTAA
CTGAAGGAGCTCTGGTTGCGAAACAACCCCATTTGAAGCATCCCTTCTTATGCTTTTAAACAATTCCTCTTT
CGCGGACTAGACTAGGGGAATTTGAAAGCTTTCTATACATCTCAGAAGTGCCTTTGAAGGCTTGTCCAACT
TGAGGTATTGAACTCTGCAATGCAACCTTCGGGAATCCCTAACTCACCCGCTCATAAACTAGATGAG
CTGGATCTTTCTGGAATCATTATCTGCCATCAGGCCCTGGCTCTTTCCAGGGTTTGTATGACCTTCAAAACT
GTGGATGATACAGTCCGAGATTCAAGTGATTGAACGGAATCCGCTTGACAACCTCAGCTCACTAGTGGAGATCA
ACCTGGCACACAATAATCTAACTATGCTGCCATCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACAT
TTACATCAACCACTTGAACGTGTAACGTGACATATCTGGCTCAGTGGTGATTAAGAGATGAGGCCCTCT
GAACAACAGCTGTTGTGCGCGGTGTAACACTCTCCCAATCTAAGGGGAGATTAACCTTGAGAGCTCGACCGA
ATTACTTACATGCTATGCTCCGGTGATTGTGGAGCCCTCGACAGCTCAATGTCACTGAAGGCATGGCAGCT
GAGCTGAAATGTGGGCTCCACATCCCTGACATCTGTATCTTGGAATCTCCAATGGAACAGCTCATGACA
TGGGGCGTACAAAGTCGGATAGCTGTGCTCAGTGATGGTACGTTAAATTTACACAAATGTAATGTGCAAGATA
CAGGCATGTACATGATATGGTGGAATTCGTTGGGAATCTACTGCTTCAGCCACCTGAACTGTTACTGCA
GCAACCACTACTCCTTCTCTTACTTTCAACCGTCACGTAGACGATTTGGAACCGCTCAGGATGAGGACG
GACCACAGATAACAATGTGGGTCCCACTCCAGTGGTGCAGTGGGAGACCACCAATGTGACCACCTCTCTCAC
CAGAGAGCAGAGGTGCGACAGAGAAACCTTCACCATCCAGTGACTGATATAAACAGTGGGATCCAGGAATT
GTGAGGCTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCAGCATCTAGCTGCAGTGTGCT
GGTCAATTTCTACAAGATGAGGAGCAGCACCATTCGCAAAACCATCACGCCCAACAGGACTGTGGAATTA
TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGGCCATCTGCCATCGCTGCTATCGAGCATGAG
CACCTAACTACTATAACTCATACAATCTCCCTTCAACCACACAACAACAGTTAACACAATAAATCAATACA
CAGTTGAGTGCATGAACCGTTATTGATCCGAATGAACCTTAAGACCAATGTACAAGAGACTCAATTAAGAA
TTTACAGAGTTACAAAAAACCAACATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTTAA
ATCTACTGTTTCAAAAAAGTGCTTTTACAAAAAAGAAAAAGAAATTTATTTATTAATAATCTTATG
TGATCTTAAGACGAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALQLLVVAGLVRAQTCPSCSCSNQFSKVIC
 VRKNLREVDPGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRYNLAMCNLREIPNLTPLIKDELDSLGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNQLSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNNPWNCNDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNFTNTVTQDTGMYTCMVSNSVGN
 TTASATLNVTAATTTFFSYFSTVTVETMEPSQDEARTTDNNVGTPVVDWETTNVTTSLTPO
 STRSTEKFTTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRRQN
 HHAPTRTVEIINVDDEITGDTPMESHLPMPIAEHEHLNHYSYKSPFNHTTTVTNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

CGCGCCGGAGCCCATCTGCCCCAGGGGCACGGGGCGCGGGGCCGGCTCCGCCCCGGCACAT
GGCTGCAGCCACCTCGCGCGCACCCGAGCGCGCGCCAGCTCGCCCGAGGTCGTCGGGA
GGCGCCGGCGCCCGGGAGCGCAAGCAGCAACTGCAGCGGGAAGCGCCCGCTCCGGGGATC
GGGACTGTCCCTCTCCTTCTCTCTTGTCTAGTTTCTACTATCTTTGGAACCTTGGGGACATCA
CACTGAGATCAAGAGAGTGTCCGAGGAAAGGTCACTTGGCCTGCCACCATCACTGGGGC
TTCCAGAAAAAGACACTCTTGATATTGAATGGCTCATTCCAGGATAAGGGAACCAAAAA
GTGTGTATCACTTACTCCAGTCGTCTATGTCTACATAAATCTGACTGAGGAACAGGAAGGCCG
AGTGGCTTTTGCTTCCAATTTCTTGCAGGAGATGCCTCTTGCAGATTGAACCTCTGAAG
TCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT
GTCACTTTAAAGTCTTATGTGAGACCATCAAGCGCCAAAGTGTGAGTTGGAAGGAGAGCTGAC
AAGAGGAATGACCTGAGCTTTGCACTGTGATGATCATCTCTGGCAGACAGCCCATTTGTATT
ACTGGCAGCGAATCCGAGAGAAGAGGGAGAGATGAAGCTCTGCCTCCCAAATCTAGGATT
GACTACAAACCCCTGGACGAGTCTGTGCGAGGAATCTTACCATTGCTCACTCTGGACTGTA
CCAGTGCACAGCAGGCAACGAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTACAGT
ATGTACAAGCATCTCGGACTGTGTTCAGGAGCAGGTACAGGCATAGTGGCTGGAGCCCTGTA
ATTTTCTCTTGTGTGTGCTGCTAATCCGAAGAAAGACAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGTCTGAAGCTCCAAAGACCCGCTCTTGTGAAACCCAGCT
CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTGTGTTCTTCTCTCCATCTCGCTCCACAGAAAT
AGTCCCTCAGCAGCCAGCGACACTGTCTCAACTGACGAGCAGCCACCCAGCGAGGCTGGCCAC
CCAGGCATACAGCCGCTATGTGGGGCCAGAGTGTGAGAGGTTCTGAACCAAAGAAAGTCCACCAT
CTAATCTGACAAAGCAGAAACCAACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA
ACGCTG**TGA**AATTACATTTGACTTGACTCCACGCTTCTCAGAGTACAGGCTCTTTGGACTC
TTCTCGTCAATGGAGCTCAAGTCACAGGCCACAACAGATGAGAGGTCACTCTAAGTAGCA
GTGAGCAATTGCAGGAAACAGATTTCAGATGAGCAATTTTCTTATACATAACCAAACGAAGAA
AGGATGTAAGCTGATTTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGG
AAGCAGGAGTCCAAATCTATTGTTGACACGAGGACCTGTGGTGAGAAGGTTGGGGAAGAGTG
AGGTGAATATACCTAAATCTTTAATGGGGATATTTGTATCAGTGGCTTTGATTCAAAAT
TTCAAGAGGAAATGGGATGCTGTTTGAATATTTCTATGCATTTCTGCAAATCTTATGGATT
ATTAGTTATTACAGAGTCAAGCAGAACCCACAGCTTATTACACCTGTCTACACCATGTAC
TGAGCTAACCACTTCTAAGAACTCCAAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC
TTCATTGTPCATAGGTTTGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA
AGAGTAATGAGTTTCTCCCACTCTATACATCAATCTCATATTTGTATTGAGCCCAAATAAC
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCTATGATT
ATGAGGATTGTTGCAACACATTAGAATATATATAATGGACATTTGTGGATTTCCTCTCAAT
CAGATGCTCTTAAGGACTTCTCTGTAGATATTTCTGGAAGGAGAAATAACAATGCTCAT
TATCAACGTCTCTTAGAAGAAATCTTCTAGAGAAAAAGGGATCTAGAAGTCTGGAAGATTA
CCCAACATACCATTATAGTCTCTTCTTCTGAGAAAACTGAAACCAAGAATTCGAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTGTAGGAAAACTCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC
ATTGCACTCTCAGCTGGGTGACAGAGCGGCACTCCGTTCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41281, pI: 8.33, NX(S/T): 3
MSLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLMTSYSGLYQCTAGNEAGKESCVVRVTYQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSSGSSSTRSTANS
ASRSQRTLSTDAAPQPLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

CGGAGGGCGGGGGAGCCCTGACACGAGGACGAGACGCCGCTTACTCTGCAGCCGCCGCCACGCGACGGCGGCCCA
CC**ATG**CGGCTCCTGCTGTGCTCTCTGCTCTCTGTCGCGGATGCTGGATTTCGCCAGCAATTTGAGTACTACTACT
CCTAGAGAGTAAATTGAAAAGGCAAGGGGAAATCGCTATTGCCATGCAAAATTTACGCTTAGTCCCAGAGA
CCAGGGAGCGCTGGACATCGAGTGGCTGATATCACCTACCGTGTAAATCAGAAGTGGGATCAAGTAAATTTTAT
ATTCTGGAGCAAAATTTATGATGACTATATCCAGATGTAAAGGCCGAGTACATTTTCAGGATTAATGATCT
AAATCTGGTGATGCATCAATAATGTACCAAGAAATTTACAACATGTCAGATATTGGCCATATCAGTCAAAAGTGAA
AAAGACTCTCGTGTCGCAAAATGAAGAAATTCATCTGGTAGTTCTTGTGAAGCTTCAGGTGGCAGATGTGACG
TTGATGGATCTGAAGAATTTGGAAGTGACTTTAAGATAAAATGTGAACCAAAAGAGGTTCACTTCCATGATACAG
TATGAGTGGCAAAATTTGTCGACTGACCAAGAAATGCCCAATCTGATGGTAGAGAAAAGTCACTCTCATCTGAT
ATCTGTAAAAAATGCCCTTCTTGAGTACTCTGGGACATACAGCTGTACAGTCAGAAAGAGGATGGGCTCTGATC
AGTGGCTGTGCGTCTAACAGTTGTGCCCTCTCAATAAAGCTGGACTAATTCAGGAGCAATATAGAAGCAT
TTGCTTGCTCTAGGCGTCAATGGCTCTATCATCTTTTGCTGTCTGAATAAAGGCCGAGAGAATAATGTAA
GGAGTTGTACATCAGATACAGGAGAGTGTGCCACTCCAAAGAGCGCTAGCTCCACTGCCAGAGTACAGCG
CGCATTAATCAATCTCCCTGGGCTCCATGTCCTCTCCAAACATGAAGAGATATTCCAAGACTCAGTATAACCAA
GTACCAAGTGAAGACTTTGAACGGGCTCTCAGAGTCGCACTCTCCCACTGCTTAAGTTCAAGTACCCCTACAA
GCTGATGGAATACAGTTCTGA**TAATAA**TATGGCATCTGAAGATCTGAAGTATTGCTATTATTGACTTTATT
AGCCCTCTAGTAAAGACTTAATGTTTTTTAAAAAAGCAAGCCAGCAGAGTTAGACAGGCTTAGAACAC
ATCTACTTTATGCAATGGCATAGACATGTAAAGTCAGATGTCATGTCAAATTAGTACAGGCCAAATTTCTGT
TAAAAAACCCCTATGTATAGTACAGCTGATAGTAAAGAGTTTATTATATTTCATAACTACCCTACAA
ATTTTAACTTTTCAATATGCATATTCTGATATGTGGCTATTAGGAAAGATCTGGTAAATGATTGTTTCAA
AGGAAAATTTAAATATTTACGTTCTGTTTAAAGTCTTTGGCTAATTAATTAATCAATAGGGAATAACCGC
TCTCTTTCCCTTTTATGTCACACACAGAACACCGCTTGTCTAGCCCTCAACATTTTATTATTGCAATCA
TGATTATGCAACAAATTTCTTAAACACGCAATGAATAGATTTCTGTATATAAATATACATACGCTCA
TAAGATTAATCTCAAAGTGTGAGAACCAATCGTCCACTCTACAGTGTCTCGTATCCAACAGAGTTGATG
ACAAATATAAATACTCAGTCCCAATATAAAACATAGGCATGACTAACTTATAAATAATTTCTCAACT
TATCAATATCTAAAGTGCTATATTTTTGAAGAAGATTATCTCAATCTCTATAAAGAAATTTGATGG
TTTGCCCACTCACTACTACATATTATGATGAAGAAATTTAACTTTAAATGTGTAGAGGTTATCTACCT
TTTTCTCAACATGACCAACCAATCAAAACAGAGTGTAGTGAGGCTACATCTGAGAGTATACATGAT
TCGGGTCAACATCGATTCCAGGAGGAGTACCCATGCTCATCGGAATGGGCAATATGTTTATTTTCTCCC
TGATTTGGATACCAAAATGGAACAGGAGGAGGATGATGATCTGATGGCCATTCCTCGATACATCTCGGCT
TTTTCTGGGCAAGAGTGGCCAACTGGAAGAGGAGTGAATAATGAAGTTCTGAATCTGTAGGGAAGAACACAT
TAAGTTAATTCAAAGGAAAAAATCACTATGATCTGATGTCAGATTTCTCATTAAGACAAAGTTAGCCACACAT
GAGATCACATCTAAGTGACCTCTTATGTGAGTCTAAATACATTAAAAACCTCATGTATAGGCGCTATAA
TGATATAACAGTGCACAAATGTTCTGAAATGATAAAGAAATGAATAACATCAACACAGTACTCTCTAAACAA
CTTCAACCAACAGAACCCAAACATGGAAACGATGGAAGCTGTGAAGCAATCTGTGAAGCATCTGTTTGTAGTCCAGTGTT
CCACAGCTGGCTAGGCAGAGTCACTTGGAGGCTTTTAAATCAAAACATTGGAGCTGGAGCGGCAATATCTCT
AGCAAACTATGTCAGAACAGAAATCAACTACCGCATGTCTTCACTATTAAATGTGGAGGTGAATGAAGCAT
TATGAACCAAGAGGAACATACAGATCACTGGAGTATTGGAAGGGGGGGTGGAGAGGGAAGGAGGAGCA
GAAAGAGTAATATTTAGTACTGCCCTCACACCTGGGTGATGAATAATATGTACACAAATCCCTGTGACACA
TGTTTACCATGTGGAACAAACCTTCATGTGTATCCCTAAACCTAAATAAAGTTAAAAAAGAAAAAARAAAAA
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA
AAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAAARAAAAA

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361

><subunit 1 of 1, 352 aa, 1 stop

><MW: 38938, pI: 7.86, NX(S/T): 3

MALLLLCFVLLCGVDFARSLSTTPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPVDGSEEIGSDFKIKCEPKESLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLRLNVPSPNKAGLIAGAIIGTLL
ALALIGLIIFCCRKKRREEKYEKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTGGTGA
 ATGGTGAAGGTGCCTGTCTAACTTTTCTGTAAAAAGAACCAGCTGCCTCCAGGCAGCCAGCC
 CTCAAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTCCGC
 CAATTTAACACCAAGAAGAAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCCTGGGTTTTACCCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCACCTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCCAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGTTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCTGCTGGAGTTCTACTTGAAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCAACAAC
 TTGTTCTCATCGTGTCAAACTGCAACCCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGCTATTCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAAGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACGTGGTTTGTTCCTGTGTCAATTTCA
 AACAGTCTCCCTTCCATGCTGTTCACTGGACATTCACGCCCTTGGCCATGGGTCCCATTCT
 TTGGCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGTAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAACTCTGCCACAGTGTGGGCGAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAACAGAGAGGGATGCTTGGATGTAAAACCTGAACCTCAGAGCATGAAAAACACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGTGGGGGTAAAGTGATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCACCCACACTCGCCAGCTCACCCCATCATCCCTTTCCCTTGGTGGCCCTCCTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAAGCTGACCTTGCTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRQLQSLWTLARFFCPPLLATASQMVMVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACACGGTCTCAGGAGATGCTGTGATTTCC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCATATCCTGTCCACATTGGAGACTCTGCAGATCATTAAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTTCTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCCAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTCCCTCTACA
TGCAGAAAACCTGCGGCAATGTCAGGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGAAGGAGATGGGGAAGGCCCTTGCAGCTGAAAGTCC
CACTGGCTGGCTCAGGCTGTCTTATTCGCTTGAAAAATAGGCAAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGCCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282
><subunit 1 of 1, 177 aa, 1 stop
><MW: 20452, pI: 8.00, NX(S/T): 2
MKLQCVSLWLLGTILILCSVDNHGLRRLISTDMHHIEESFQEIKRAIQAKDTFPNVITLST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCAGCATGTTGGGGGCCGCCT
CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTGAC
CCGAGAACTGCAGGTTCCAACACCAGACGCTGGAAAACGGGTACGACGCTACCACTCTCC
TCAGTATCACTTCCTGGTCAGTCTGGGCCGGGCGCAAGAGAGCCTTCCTGCCAGGCATGAACC
CACCCCGTACTCCAGTTCCCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCTGAACGT
GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCCTCCTGTTACAGGAGCTCCCGAGCG
CCGAGGACAACAGCCCGATGGCCAGTGACCATTAGGGTGGTCAGGGCGGTGAGTGAAC
ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTATCTAGGGTCG
CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRRLWVCALCSCMSVLRAYPNASPLLGSWSGGLIHLYTATARNSYHLQIHKNGHVD
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYLCMDFRGNI FGSHYFDPENCRFQHQTLNGY
DVIYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:

Signal peptide:

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGGCTCTGCCCTTTTCTTCTCTGTGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGCGAGAGCAGACACTGCGATGACAAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCGGGGCCACGCCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCTCAACCCAGCCGGCCCCATTCCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCCAACTTCATGGTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGCGAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTCAGACCATCACAGGCAGTGATCCCGAGGAAGCCATCTTTGACACCCCTTTGCACCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCAGAGAGCAGTGCCCTCTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCTCAGAGAGCAGCGCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTCAT
 GGTCCCCGGGATCTGATGTCACCTCTCTCGTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGCAGCATCACAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCTCTGTCCACCTCCGATCCACAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCCAGAGTCAGCTGCACCTCATGCCAGGTTGGGACCCCACTCCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCTCAGTGAGGCTCTGGTCA
 CAGTTAGCAGGAATCCCCTGGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGCTGGGTACGAGTGGGCAAAACAACCTC
 CTTTGCTGGGAGCTCTGCTTCTCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTCACCC
 CTTCAGAGACACCGACCATTGACATCGCAACCAAGGGGCCCCTTCCCACAGCAGGGACCCCT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCACAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCCGGAC
 GAGGCCGACCACAGACG**TGAG**GTGCAAGGTGAAATGGAGGTTTCTCTCTGCGGCTGAGTG
 TGGCTTCCCCGGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGGAATCCACGCCACCGGCTCACTTCCAGGTCTCTTACTGCGTGTGAGAGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCAACCCAGATGTGGCAACAGGACCCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTACCTGTTCCAGAGGTGTCTTTGGAACCTACCTTG
 CACATGTTCTGTGTTTCACTAAAGAGAGACCTGATCACCATCTGTGTGCTTCCATCCTGCA
 TTAAATTTCACTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRRADTAMTTDDTEVPAMTLAPGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPARETRSFTKTSNFMVLIATSVETSAASGSPEGAGM
 TTVQTITGSDPEEAI FDTLTCDSDSEEAKTLTMDILTLAHTSTEAKGLSSESSASSDGPHPV
 IPTSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTLAEALVTVTNI
 EVINCSITEIETTTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTLGALVTVSRNPLEETSALSVEFPSY
 VKVSGAAPVSIEAGSAVGKTTSFAGSSASSYSPSEALKNFTPSETPTMDIATKGFPPTSRD
 PLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKPQQPRPRLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP-and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCCGCGCGGATTGCGCGGTCTTCCCGCGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTCTGTGCAGCCTTCTTAAAGCAAACTAAGACCAGAGGGAGGATTAT
 CATTGACCTTTGAAGACCAAACTAAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGAG
 CTTGACTTACACTTTTGGTAATAATTGTCTCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACTTCAACTCAAGAAGACTGCATTAATTTCTGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCTGTCCATTGAACACAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTCTTACATGGCCAATTTTCAACAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCCAACGATATCTCATGGAGAGACACACTTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAAAATGTGAGTGCGCTCCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCCACGACCTCATTTTCTACAGTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTAGGCACCTACGGACTCGAAGGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTGAACACAGGGAATGTGTATAACCTTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTGGGAAGGT
 AGGGAGGCCAGTCCAGGCAGTTCTCTCCAGGGCAGTGTTCAGAAAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGGTGATAGGCC
 TCGTCTCTCGGGTGAATCCTTTCCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGCTCTTAATTCATT
 TAGTAACCAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
 TATTTTGAAGACAGGAAATGCCCTTCTGCTTTCTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCCACCGCAACCTCCGTCTC
 CTGGGTTCAAGCGATTTCTCTGCTCAGCCTCTTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACCTGGGTGATTTTGTATTTTGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCTCAAACCTCTGACCTAGTGATCCACCTCTCGGCTCCCAAAGTGCTGGGATTACAGG
 CATGAGCCACACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTGAGAAGGAATGAAGTG
 GGAACCAAAATTAGTAATTTTGGGTAATCTGTCTCAAAATATTAGCTAAAAACAAAGCTCT
 ATGTAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTTCACTGGCTTTTATGCAAA
 GAAACAGGTTAGACATCTAGGTTCCAATTCATTACATTTCTGGTTCAGATAAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTGCTTTCTTTTATATGGATTCTTTTAAACCTTATT
 CCAGATGTAGTTCCTTCCAATTAATATTGAATAAACTTTTGTACTCAA

FIGURE 328

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
><subunit 1 of 1, 431 aa, 1 stop
><MW: 46810, pI: 6.45, NX(S/T): 6
MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMI F DTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHSTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFKEKWLIGSLLFGVLFVLVIGLVLLGRILSESLRRKRYSLDYLINGIYVDI
```

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCACGCGGTGCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTTGCGTCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT
 GGGATCCTCTTCTCGTCTGCTCTGGCACCATCTATGCAGAGAAGAAGGCCAGGAGCAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCTGTGGA
 ACCTCACCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCTGCTTTCCAGGACCTGCTGTCTCCCTCCCTCTTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCTCGAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGTCTTACCCTGGCAGCCACCACAGCCAAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC
 AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGACAGC
 TGGACTCCACCTCAGCAGAGGACACCACTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCACAG
 GTGTCCATCCCGATGGTCCGCATCTAGGCCAGTCTGGTGTCTGCTGAGCCTTCTGTGAGC
 CGCAGGCCTGATCGCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTCTTGGCTCTCAGCCTTGACTGCGGAGGAAAGGAAGCC
 CCTTCCAGGCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA
 GCTGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTCGCCGGACTCCAGGGCTCTCCCCACCTCCCCAGGCTCTCCTCTTGCATGTTCCCA
 GCCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCTTGTCTTCCGGTGC
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGCAGAGTACCAGGCTGCTGACCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC
 CTCATGCCCAGTGTGCGGACCTGCCTTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCGTCTCAGACTTAGTCCCAGGCTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACACCTGCATCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCCTGGCCCCACCAAGACCCACCAAAACCATTCTCTGGGCTTGGTGCAG
 GACTCTGAATTTCAACAATGCCAGTGACTGTCGCACTTGAGTTTGAAGGCCAGTGGGCGCTG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACTCGCC
 CAATAGATCTGCTCTGTCTGCGACACAGATCCACGTGGGGACTCCCTGAGGCCTGCTAAG
 TCCAGGCCTTGGTCAGGTGACGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCTTTNCCATTGGCCCTCCCTGGNCCATGCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACCTTTGGCTTCTTCTTGTCTGGAAGGGTTACTTGCCATATGGGTTCTGGTGGCTAGAGA
 GAAAAGTGAAGAACAGAGTGCACGTAGGTGTCTAACACAGAGGATGAGGAAGACAGGCGCG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGTGGTGGTAAAGTA
 GCACAACCTACTATTTTTTTCTTTTTCCATTATTATTGTTTTTAAGACAGAATCTCGTGTCT
 GCTGCCAGGCTGGAGTGCAGTGGCAGCATCTGCAAACTCGCCCTCTGGGTTCGAAGTATT
 CTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGACCACCACCTTGGCTAATT
 TTTGACTTTTAGTAGAGATGGGGTTTACCATTGTTGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAAATGAGCCTCCTGCTTCACTCTCCCAAAATGGCGGATACAGGATGAGCCACTGTG
 TCTGGCCCTATTTCCTTTAAAGAGTGAATAAGAGTTGTTTCAATGATGCAAACTTGGAAAG
 ATGGAGGAGAAAAAGGAGGAGAAAAAATGTCACCCATAGCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTACTTCTTCCACTTTTTCTTCTTACATAAATTTGCCGGTGTCTT
 TTTACAGAGCAATTTATCTGTATATACAACCTTTGTATCCTGCCTTTTCCACCTTATCGTTCC
 ATCACCTTTATTCAGCACTTCTCTGTGTTTACAGACCTTTTATAAATAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALLEGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD ELLISLFV
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQKGTGAEAPPLPG
TSQYGHERTSQYTGTSPPHATSPPPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI
LAPVLVLLSLLSAAGLIAFCSHLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128